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Qy	902	AATCTGAA	ACTTCCACGCCCTCTCAGAAACCTCTATAAGGATCGAA	TGGCCCAAGTACCAG	961	
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Db	1020	CTGTCTCC	TCTGTAAGATGACACTGTAACCTCCAGGTGAAGACGAGGCC	CAGCAGCCT	1079	
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DB	1800	TCCTTTCGAACCTCTTCCATCAAGAGCCCAAGGCCCTCTTCGCCATCTCTCAGGAAGGT	1859
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RESULT 5
AL578990/
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

Accession	Length	Organism	Library	EST	Date
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AL578990		Homo sapiens HELA CELLS	COT 25-NORMALIZED	Homo sapiens	
		cDNA clone CS0DK012YC22	3-PRIME,	mRNA sequence.	

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1014)
 REFERENCE Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 AUTHORS Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 16, 2001 this sequence version replaced gi:12943595.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 6590.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DK012BB11NP1&cluster=6590.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DK012BB11NP1.
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 /note="1st strand cDNA was primed with a NotI-oligo(dt)
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 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 354 a 184 c 170 g 296 t 10 others
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 cDNA clone CS0DK012YC22 5-PRIME, mRNA sequence.
 ACCESSION AL556858
 VERSION AL556858.2 GI:31278659
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1045)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12899909.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 6590.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DK012BB11NP1&cluster=6590.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DK012BB11NP1.
 Location/Qualifiers
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCWSPO1 6 vector. Library was normalized."
BASE COUNT      334 a 172 c 205 g 313 t      21 others
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Query Match      25.0%; Score 927.6; DB 9; Length 1045;
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Matches 947; Conservative 19; Mismatches 14; Indels 2; Gaps 2;
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RESULT 7
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ACCESSION BM909158
VERSION BM909158.1 GI:19359537
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1075)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI904 row: j column: 10
High quality sequence stop: 696.
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in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
Note: this is a NIH-MGC Library."
BASE COUNT 354 a 256 c 258 g 207 t
ORIGIN

Query Match 24.2%; Score 898.2; DB 12; Length 1075;
Best Local Similarity 96.6%; Pred. No. 5.2e-106;
Matches 961; Conservative 0; Mismatches 28; Indels 6; Gaps 4;
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Db	661	ATTCATAAATGGAGCAAAAGGAGAAATGTGCCCCAGGTCTCTGAGTCTGCATCACCAT	720
Qy	1094	CAGGAAGGGGAAAGATTTCTGCAAAATGAGAAATAGCCTGGGAGTCCGTTCCACCCCTGCC	1153
Db	721	CAGGAAGGGGAAAGATTTCTGCAAAATGAGAAATAGCCTGGGAGTCCGTTCCACCCCTGCC	780
Qy	1154	GAAGATGACTCCCGTACTCCAGGTTAAGAGTGAAGTTCACAGCTGTCCATCCCAAG	1213
Db	781	GAAGATGACTCCCGTACTCCAGGTTAAGAGTGAAGTTCACAGCTGTCCATCCCAAG	840
Qy	1214	CCACTAAGTCAGATTCAGAGCCCTCCAG-TCTTTCTGAAAGTTCTCTCCCAAGCAAT	1272
Db	841	CCACTAAGTCAGATTCAGAGCCCTCCAGTCTCTTTCTGAAAGTTCTCTCCCAAG-AAT	899
Qy	1273	GAAGAAGTTTCAGGCACCTCGAAGAGACCTCGGTGGAA--TGTGAGAGACAGTCTA	1329
Db	900	GAAGAAGTTTCAGGCACCTCGAAGAGACCTCGGTGGAA--TGTGAGAGACAGTCTA	959
Qy	1330	TCCATGG-AGCGTCTCTTGCCACCCAGCAGGTG 1363	
Db	960	TCCCATGGAAGCGTCTCTTGCCCAACCAAGAGGG 994	
RESULT 8			
BI871114			
LOCUS			
DEFINITION			
603394291F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5404054 5',			
mRNA sequence.			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Homo sapiens (human)			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 880)			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			

Email: egabs-i@mail.nih.gov			
Tissue Procurement: ATCC			
cDNA Library Preparation: Life Technologies, Inc.			
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Incyte Genomics, Inc.			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LLNL at:			
http://image.llnl.gov			
Plate: LLAM12030 row: f column: 23			
High quality sequence stop: 799.			
FEATURES			
source			
1..880			
/organism="Homo sapiens"			
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/db_xref="taxon:9606"			
/clone="IMAGE:5404054"			
/tissue_type="adenocarcinoma, cell line"			
/lab_host="DH10B (phage-resistant)"			
/clone_lib="NIH MGC 90"			
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;			
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.			
Average insert size 1.7 kb. Library enriched for			
full-length clones and constructed by Life Technologies.			
Note: this is a NIH MGC Library."			
BASE COUNT			
ORIGIN			
308 a 136 c 181 g 255 t			
Query Match			
21.8%; Score 806.8; DB 12; Length 880;			
Best local Similarity 96.7%; Pred. No. 3e-94;			
Matches 845; Conservative 0; Mismatches 27; Indels 2; Gaps 2;			
Qy	2124	GGAGAGAGTAAAGGAGTCTAGTTTGGAGATGAGAGATGAGAGATGAGAGATGAGAGATG	2183
Db	1	GGAGAGAGTAAAGGAGTCTAGTTTGGAGATGAGAGATGAGAGATGAGAGATGAGAGATG	60
Qy	2184	GTGCAGACTCCGATGAAGATGATAACAGCTTCTCTCAACAAACAACTCTCCACAGAACCCCA	2243
Db	61	GTGCAGACTCCGATGAAGATGATAACAGCTTCTCTCAACAAACAACTCTCCACAGAACCCCA	120
Qy	2244	AGTCTCTGAATTTGGTTCGAGTTTGTAGACAAACACCTTTGCTGAAGAAATTCACCTACTCAGA	2303
Db	121	AGTCTCTGAATTTGGTTCGAGTTTGTAGACAAACACCTTTGCTGAAGAAATTCACCTACTCAGA	180
Qy	2304	ATCAGAAATCCAGGATGTGGAACTCTGGAGGGAGAAAGTGTCAAGAGCTCTCTGTGG	2363
Db	181	ATCAGAAATCCAGGATGTGGAACTCTGGAGGGAGAAAGTGTCAAGAGCTCTCTGTGG	240
Qy	2364	AAGAACAGATAAAGAGAAATCCGTATTATGATGAGGATGAGGATGAGAGTGAACAATTG	2423
Db	241	AAGAACAGATAAAGAGAAATCCGTATTATGATGAGGATGAGGATGAGAGTGAACAATTG	300
Qy	2424	CAATGATGCTGGGCTTAAATTCATGTTAGTGTAGCGAGCCACTGCCCTTTGTCAAAAT	2483
Db	301	CAATGATGCTGGGCTTAAATTCATGTTAGTGTAGCGAGCCACTGCCCTTTGTCAAAAT	360
Qy	2484	GTGATGCACATAGCAGGTATCCAGCATGAAATGTAATTTACTTGGAAAGTAACTTTGGA	2543
Db	361	GTGATGCACATAGCAGGTATCCAGCATGAAATGTAATTTACTTGGAAAGTAACTTTGGA	420
Qy	2544	AAAGAAATTCCTTCTTAAATCAAAAACAAAACAAAACAAAACAAAACAAAACAAAAC	2603
Db	421	AAAGAAATTCCTTCTTAAATCAAAAACAAAACAAAACAAAACAAAACAAAACAAAAC	480
Qy	2604	ACTAGAGATAACTTTACTTTAAATTCCTTAAATTCCTTAAATTCCTTAAATTCCTTAAAT	2663
Db	481	ACTAGAGATAACTTTACTTTAAATTCCTTAAATTCCTTAAATTCCTTAAATTCCTTAAAT	540
Qy	2664	AAGGCTTGTAAGTGGGAAATATTCACCTGATAATAGCCAGATTTCTACTGTAATCCCA	2723
Db	541	AAGGCTTGTAAGTGGGAAATATTCACCTGATAATAGCCAGATTTCTACTGTAATCCCA	600
Qy	2724	AAAGCAATATTAAAGTAGATGATGATTAGTAGTATATTGTACACACTATTTTGGAAAT	2783

Db 601 AAAGCAATATTAAGGTAGATGATTAGTAGTATATATGTTACACACTATTTTGAAT 660

QY 2784 TAGAGACATACAGAGGAATTTAGGGCTTTAAACA-TTACGACTGAATGCACCTTTAGTA 2842

Db 661 TAGAGACATACAGAGGAATTTAGGGCTTTAAACA-TTACGACTGAATGCACCTTTAGTA 720

QY 2843 TAAAGGACACAGTTTGTATATTTTAAATGAATACCAATTAA-TTTTGTAGTATTTACC 2901

Db 721 TAAAGGACACAGTTTGTATATTTTAAATGAATACCAATTAA-TTTTGTAGTATTTACC 780

QY 2902 TGTAAAGAGATTTATTTAGTCTTTTAAATTTTAAATTTTAAATTTTCTGCTGTGATATAT 2961

Db 781 TGTAAAGAGATTTATTTAGTCTTTTAAATTTTAAATTTTAAATTTTCTGCTGTGATATAT 840

QY 2962 GAGGAATTTACTACTTTATGTCCTGCTCTCTAAA 2995

Db 841 GCAGGAATTTACTACTTTATGTCCTGCTCTCTAAA 874

RESULT 9

CD171644

LOCUS

DEFINITION AGENCOURT 14065890 NIH_MGC_180 Homo sapiens cDNA clone

IMAGE:30378885 5', mRNA sequence.

CD171644

CD171644.1 GI:30852393

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 884)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: NDA445 row: g column: 22

High quality sequence start: 16

High quality sequence stop: 648.

Location/Qualifiers

1. 884

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"

/clone="IMAGE:30378885"

/clone_lib="NIH_MGC_180"

/notes="Organ: Testis; Vector: pCMV-Sport6.1; Site 1: NotI; Site 2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC library."

BASE COUNT 306 a 168 c 225 g 185 t

ORIGIN

Query Match 21.7%; Score 802.4; DB 14; Length 884;

Best Local Similarity 98.4%; Pred. No. 1.1e-93;

Matches 842; Conservative 0; Mismatches 11; Indels 3; Gaps 3;

QY 1730 TGCCACCCCCCACTGAATTTGGAAGTTCAGGAAGTGCCTTGAGCAAGGGATCAAAATG 1789

Db 27 TGCCACCCCCCACTGAATTTGGAAGTTCAGGAAGTGCCTTGAGCAAGGGATCAAAATG 86

QY 1790 TCAAGCCCAAAATGGCTCTCTGAAGACGAAATCAGCAAGCCCAAGTTCCTCAGGATGTC 1849

Db 87 TCMAAGCCCAATATGGCTCTCTGAAGACGAAATCAGCAAGCCCGAAAGTTCCTCAGGATGTC 146

QY 1850 GATCTAGATCTGAAGAAGCTAAAGACGATCTTCTTCACTGAAGAAAGAGCGCCCATTC 1909

Db 147 GATCTAGATCTGAAGAAGCTAAAGACGATCTTCTTCACTGAAGAAAGAGCGCCCATTC 206

QY 1910 ACTGTAGCAGCTTCTATTTCAAAGCACCTCTGTCAAGAGCCCCAAAACTGTGTCCTCCACCT 1969

Db 207 ACTGTAGCAGCTTCTATTTCAAAGCACCTCTGTCAAGAGCCCCAAAACTGTGTCCTCCACCT 266

QY 1970 ATCAGAAAGGCTGGAGCATGTTCAGAGCAGAGTGAAGAGTCTGTGGTGGAGAGGTTGCA 2029

Db 267 ATCAGAAAGGCTGGAGCATGTTCAGAGCAGAGTGAAGAGTCTGTGGTGGAGAGGTTGCA 326

QY 2030 GAAAGGAAACAAGTGGAAATGCCAAGGCTTCTAAGACAAATGGGAATGTGGAAAAACA 2089

Db 327 GAAAGGAAACAAGTGGAAATGCCAAGGCTTCTAAGACAAATGGGAATGTGGAAAAACA 386

QY 2090 ACCTGGCAAAACAAGAAATCTTAAAGGAGAGACAGGAGAGAGTAAGGAAGTTCATAGT 2149

Db 387 ACCTGGCAAAACAAGAAATCTTAAAGGAGAGACAGGAGAGAGTAAGGAAGTTCATAGT 446

QY 2150 TTGGAGATCGAATGAGAAATCTTGTAGAAAAATGGTGCAGACTCCGATGAAGATGATAAC 2209

Db 447 TTGGAGATCGAATGAGAAATCTTGTAGAAAAATGGTGCAGACTCCGATGAAGATGATAAC 506

QY 2210 AGCTTCTCTCAAAACAACAATCTCCACAAGAACCCAAAGTCTCTGAATTTGGTCGAGTTTGT 2269

Db 507 AGCTTCTCTCAAAACAACAATCTCCACAAGAACCCAAAGTCTCTGAATTTGGTCGAGTTTGT 566

QY 2270 GACACACCTTTGCTGAAGAAATTTCACTCTCAGAAATCAGAAATCCAGGATGTGGAATC 2329

Db 567 GACACACCTTTGCTGAAGAAATTTCACTCTCAGAAATCAGAAATCCAGGATGTGGAATC 626

QY 2330 TGGAGGGAGAAAGTGGTCAAAAGAGCTCTCTGTGGAAAGAACAGATAAAGAGAAATCGGTAT 2389

Db 627 TGGAGGGAGAAAGTGGTCAAAAGAGCTCTCTGTGGAAAGAACAGATAAAGAGAAATCGGTAT 686

QY 2390 TATGATGAGGATGAGGATGAAGAGTGAACAAATGCAATGATCTGGGCTTTAAATTCATG 2449

Db 687 TATGATGAGGATGAGGATGAAGAGTGAACAAATGCAATGATCTGGGCTTTAAATTCATG 746

QY 2450 TTAGTGTAGGAGGACCTGCTGCTTGTGCAAAATGTCATGCACATAGCAGGATCCCA 2508

Db 747 TTAGTGTAGGAGGACCTGCTGCTTGTGCAAAATGTCATGCACATAGCAGGATCCCA 806

QY 2509 GCATCAAAAT-GTAATTTTACTTTGGAAGTAACTTT-GGAAAGAAATTCCTTCTTAAATCAA 2566

Db 807 GCATCAAAATGGAATTTTACTTTGGAAGTAACTTTGGGAAAGAAATTCCTTCTTAAATTCG 866

QY 2567 AAACAAAACAAAAA 2582

Db 867 AAACAAAACAAAAA 882

RESULT 10

BM914155

LOCUS

DEFINITION BM914155.1 1142 bp mRNA linear EST 12-MAR-2002

AGENCOURT_6608184 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5479040

5', mRNA sequence.

BM914155

BM914155.1 GI:19364534

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1142)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1999 row: k column: 09
High quality sequence stop: 678.
Location/Qualifiers
1. 1142
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/clone="IMAGE:5479040"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_98"
/note="Organ: brain; vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 376 a 282 c 276 g 208 t

ORIGIN

Query Match 21.3%; Score 787.8; DB 12; Length 1142;

Best Local Similarity 94.9%; Pred. No. 7.4e-92;

Matches 890; Conservative 0; Mismatches 37; Indels 10; Gaps 6;

QY	347	GTGTTAAAGAGAACTGGGAGCAACCCAGGCTGGGAGCAGAGTCTCACACAGACTCTCTA	406
Db	1	GTGTTAAAGAGAACTGGGAGCAACCCAGGCTGGGAGCAGAGTCTCACACAGACTCTCTA	60
QY	407	CGGAACAGCAGCACTAGATTAGGCACAGACAGACCATCTCTGTTGAAGTCACAAAGC	466
Db	61	CGGAACAGCAGCACTAGATTAGGCACAGACAGACCATCTCTGTTGAAGTCACAAAGC	120
QY	467	CACGCTGCTTCTGGAGCCAAAGCTGACCAAGAAACAAATCCACCCAGATCTTAGACTC	526
Db	121	CACGCTGCTTCTGGAGCCAAAGCTGACCAAGAAACAAATCCACCCAGATCTTAGACTC	180
QY	527	AGGTCACTCTGTAGAGCCCTCTGTAGAGTGCATATCCCAATCAAGGACGTTAGGAT	586
Db	181	AGGTCACTCTGTAGAGCCCTCTGTAGAGTGCATATCCCAATCAAGGACGTTAGGAT	240
QY	587	CTTAAAGACCACTCAACAGAAAGTAAAAAATGGAATAATGCTAGGAGATCCAGGCAT	646
Db	241	CTTAAAGACCACTCAACAGAAAGTAAAAAATGGAATAATGCTAGGAGATCCAGGCAT	300
QY	647	GAAGTAGAAAAATCAGAAATCAGTGAAGAACACAGATGCTTCGGGCAAAATAGAGAAATAT	706
Db	301	GAAGTAGAAAAATCAGAAATCAGTGAAGAACACAGATGCTTCGGGCAAAATAGAGAAATAT	360
QY	707	AATGTTCCGCTCAGACAGCTTAAGATGATGTTTGAAGAAAGTGAACCACTCAAACTAAG	766
Db	361	AATGTTCCGCTCAGACAGCTTAAGATGATGTTTGAAGAAAGTGAACCACTCAAACTAAG	420
QY	767	ATTCTCCGGGCCCCAAGCCGAAGTGCAGTGGAGGAGATCTCTGAAGAACAGCTATTCT	826
Db	421	ATTCTCCGGGCCCCAAGCCGAAGTGCAGTGGAGGAGATCTCTGAAGAACAGCTATTCT	480
QY	827	CTAGATGACCTGGAAATAGGCCAGGTCAGTTGTTCATCTTCTACATTTGACTCGGAAAA	886
Db	481	CTAGATGACCTGGAAATAGGCCAGGTCAGTTGTTCATCTTCTACATTTGACTCGGAAAA	540
QY	887	AATGAGATACGAAATCTGGAACTCCAGCTCTCAGAAACCTCTATAAAGATCGA	946
Db	541	AATGAGATACGAAATCTGGAACTCCAGCTCTCAGAAACCTCTATAAAGATCGA	600

QY	947	ATGCCCAAGTACCAGGCAGCTGTGTCCAAACAAAGCAGCTCAACCAACTATACAAATGAG	1006
Db	601	ATGCCCAAGTACCAGGCAGCTGTGTCCAAACAAAGCAGCTCAACCAACTATACAAATGAG	660
QY	1007	CTCAAGCCAGTGGTGGCAAAATCAAAATTCATAAAATGGACAAAGGAGATGTGCC	1066
Db	661	CTCAAGCCAGTGGTGGCAAAATCAAAATTCATAAAATGGACAAAGGAGATGTGCC	720
QY	1067	CCAGGT-CTGAGGTCTGCATCACCATCAGGAAGGGGAAAAGATTCTGCAAAATGAGAA	1125
Db	721	CCAGGTCTCCCTGAGGTCTGCATCACCATCAGGAAGGGGAAAAGATTCTGCAAAATGAGAA	780
QY	1126	TAG-CTGCGCAGTCCGTTCCACCCC--TCCGGAAGATGACTCCCGTACTTCCAGGTT--	1180
Db	781	TAGCCCTGGCAGTCCGTTTTCACCCCCTGCGGAAATATGACTCCCGGACTTCCACAGGTTA	840
QY	1181	-AAGATGAGGTTCAACAGCCTGTTCATCCCAA-GCCATTAAGTCCAGATT--CCAGAGC	1236
Db	841	AAAGGGAGGTTTCAACAGGCTGGCCATCCCAAGGCCCTTAAGTCCAGATTTCCAAAGGC	900
QY	1237	CTCCAGCTCTTCTGAAAGTTCTCCTCC	1263
Db	901	CTCCAGCTCTTCTGAAAGTTCTCCTCC	927

RESULT 11

BM721370

LOCUS

BM721370 810 bp mRNA linear EST 01-MAR-2002
UI-E-E01-aib-f-18-0-UI.r1 UI-E-E01 Homo sapiens cDNA clone
UI-E-E01-aib-f-18-0-UI 5', mRNA sequence.

ACCESSION

BM721370

VERSION

BM721370.1 GI:19041235

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 810)

AUTHORS

Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE

Normalization and subtraction: two approaches to facilitate gene

JOURNAL

Genome Res. 6 (9), 791-806 (1996)

MEDLINE

9704477

PUBMED

8889548

COMMENT

Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).

Seq primer: M13 Reverse.

Location/Qualifiers

1. 810

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-E01-aib-f-18-0-UI"
/tissue_type="fetal eye"
/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
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/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
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UI-E-E01 is a normalized cDNA library containing the
following tissue(s): fetal eye. The library was
constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (d)18 tail. The sequence tag for this library is CGCCTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."										
BASE COUNT	277 a	124 c	155 g	251 t	3 others					
ORIGIN										
	Query Match	20.9%;	Score 775.4;	DB 12;	Length 810;					
	Best Local Similarity	98.6%;	Pred. No. 3.3e-90;							
	Matches 801;	Conservative 0;	Mismatches 9;	Indels 2;	Gaps 2;					
QY	2308	GAATATCCAGGATGTGGAAC	TCTCGGAGGGAGAAGTGGT	CTCTGTGGAAGA	2366					
Db	1	GAATATCCAGGATGTGGAAC	TCTCGGAGGGAGAA-TGGTCAAA	GAGCTCTCTGTGGAAGA	59					
QY	2368	ACAGATAAAGAGAATCGTATT	TATGATGAGGATGAGGATGAACAGT	GCACAAATTCGAAT	2427					
Db	60	ACAGATAAAGAGAATCGTATT	TATGATGAGGATGAGGATGAACAAATTCGAAT	119						
QY	2428	GATGCTGGGCCTTAAATTCAT	GTGTAGTGTAGCGAGCCACTGC	CCCTTTGCATAATCTGA	2487					
Db	120	GATGCTGGGCCTTAAATTCAT	GTGTAGTGTAGCGAGCCACTGC	CCCTTTGTCAAAATGTGA	179					
QY	2488	TGCACATAAGCAGGTATCCG	AGCATGAAATGTAATTTACTTGG	AAAGTAACCTTTGGAAAAG	2547					
Db	180	TGCACATAAGCAGGTATCCG	AGCATGAAATGTAATTTACTTGG	AAAGTAACCTTTGGAAAAG	239					
QY	2548	AATTCCTTCTTAAATCAAAA	ACAAAAACAAAAACACAAAAAC	ACATCTCTAAATCTA	2607					
Db	240	AATTCCTTCTTAAATCAAAA	ACAAAAACAAAAACACAAAAAC	ACATCTCTAAATCTA	299					
QY	2608	GAGATAACTTTTACTTAAAT	CTTTCATTTTAGCAGTGTATG	TATGCATAAGTGTGTAAGG	2667					
Db	300	GAGATAACTTTTACTTAAAT	CTTTCATTTTAGCAGTGTATG	TATGCATAAGTGTGTAAGG	359					
QY	2668	CTTGTAAC	TGGGAAATATTCACCTCAT	AATAGCCAGATTCTACTGTAT	2727					
Db	360	CTTGTAAC	TGGGAAATATTCACCTCAT	AATAGCCAGATTCTACTGTAT	419					
QY	2728	GCAATATTAAGGTAGATAG	TATAGTATATTGTTACACACT	ATTTTTGGAAATAGA	2787					
Db	420	GCAATATTAAGGTAGATAG	TATAGTATATTGTTACACACT	ATTTTTGGAAATAGA	479					
QY	2788	GAAACATACAGAAAGAAAT	TTAGGGGCTTTAAACATTAAC	AGCTTAACTGTATATAAG	2847					
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QY	2848	GGCACAGTTTGTATATTTT	TAAATGAAATACCAATTTA	ATTTTATTTAGTATTTACTCTGTAA	2907					
Db	540	GGCACAGTTTGTATATTTT	TAAATGAAATACCAATTTA	ATTTTATTTAGTATTTACTCTGTAA	599					
QY	2908	GAGATTTATTAGTCTTTAA	ATTTTATTTTAGGTTAAATTT	CTCTGTGATATATATAGGAA	2967					
Db	600	GAGATTTATTAGTCTTTAA	ATTTTATTTTAGGTTAAATTT	CTCTGTGATATATATAGGAA	659					
QY	2968	TTTACTACTTTATGTCGT	CTCTCTAACTACATCTG	GAACCTCGAGTCTCGAGGTATAA	3027					
Db	660	TTTACTACTTTATGTCGT	CTCTCTAACTACATCTG	GAACCTCGAGTCTCGAGGTATAA	719					
QY	3028	TACAAACAGAGCACTTTT	TGAGGCAATGAAAAACCA	ACCTTACACTCTTCGGTCTTTAGAG	3087					
Db	720	TACAAACAGAGCACTTTT	TGAGGCAATGAAAAACCA	ACCTTACACTCTTCGGTCTTTAGAG	778					
QY	3088	AGATCTGCTGTCTCCAAA	ATAAGCTTTTGTAT	3119						
Db	779	AGATCTGCTGTCTCCAAA	ATAAGCTTTTGTAT	810						

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 828)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Pietro Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1701 row: m column: 04
High quality sequence stop: 803.
Location/Qualifiers
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/organism="Homo sapiens"
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/notes="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',
size-selected for average insert size 2.3 kb and
normalized to 100 ng. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
276 a 155 c 222 g 165 t

BASE COUNT
ORGIN

Query Match
Best Local Similarity 97.8%; Score 766; DB 12; Length 828;
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VERSION BG676749.1 GI:139008146
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 781)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10599 row: p column: 03
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/clone_lib="NCI_CGAP_Skn4"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
239 a 142 c 132 g 268 t

BASE COUNT
ORIGIN

Query Match
Best Local Similarity 20.6%; Score 764.2; DB 10; Length 781;
Best Local Similarity 99.5%; Pred. No. 9.1e-89;

Matches 777; Conservative 0; Mismatches 3; Indels 1; Gaps 1;			
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Db	781	A 781	

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Job time : 7194 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2004, 09:51:46 ; Search time 199 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	362	9.8	586	3	US-09-385-982-139
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6	126.4	3.4	710	4	US-09-016-434-701
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ALIGNMENTS

RESULT 1

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; Sequence 45, Application US/09620312D

; Patent No. 6569662

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyan

; APPLICANT: Chen, Rui-hong

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wehrman, Tom

; APPLICANT: Xue, Aidong J.

; APPLICANT: Yang, Yonghong

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Zhou, Ping

; APPLICANT: Ma, Yungqing

; APPLICANT: Wang, Dunrui

; APPLICANT: Wang, Zhiwei

; APPLICANT: John Tillinghast

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. 6569662el Nucleic Acids and

; FILE REFERENCE: Polypeptides

; CURRENT APPLICATION NUMBER: US/09/620,312D

; CURRENT FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: 09/552,317

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: 09/488,725

; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 1105

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; LENGTH: 2905

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; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (173)...(2452)

US-09-620-312D-45

Query Match

Best Local Similarity 75.5%; Score 2797.6; DB 4; Length 2905;

Matches 2842; Conservative 0; Mismatches 24; Indels 10; Gaps 2;

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RESULT 2
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; Sequence 139, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; EARLIER FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 139
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(586)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-139
```

Query Match

9.8%; Score 362; DB 3; Length 586;

```
Best Local Similarity 100.0%; Pred. No. 1-9e-84;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3137 GTACTCCAAATGATTGCTTTCTTTCTGGTGATATCTGTCTCTCATAATTACTGAAAG 3196
Db 363 GTACTCCAAATGATTGCTTTCTTTCTGGTGATATCTGTCTCTCATAATTACTGAAAG 304
QY 3197 CTGCAATATTTTAGTAATACCTTCGGGATCACTGTCCCCCATCTTCGTGTTAGAGCAAA 3256
Db 303 CTGCAATATTTTAGTAATACCTTCGGGATCACTGTCCCCCATCTTCGTGTTAGAGCAAA 244
QY 3257 GTGAAGAGTTTTAAAGGAGGAAGAAGAACTGCTTTACACCACTTGAGCTCAGACTC 3316
Db 243 GTGAAGAGTTTTAAAGGAGGAAGAAGAACTGCTTTACACCACTTGAGCTCAGACTC 184
QY 3317 TAAACCCCTGATTTTCCCTTTATGATGTCCCTTTTGTAGACACTAAATTTTAAATACTTAC 3376
Db 183 TAAACCCCTGATTTTCCCTTTATGATGTCCCTTTTGTAGACACTAAATTTTAAATACTTAC 124
QY 3377 TAGCTCTGAATATATTGATTTTATCAGATATTTCTCAGGTTGAAAATTAACCAACTAT 3436
Db 123 TAGCTCTGAATATATTGATTTTATCAGATATTTCTCAGGTTGAAAATTAACCAACTAT 64
QY 3437 AGGCTTTTCTTGGGATGATTTTCTAGTCTTAAGTTTGGGACATTAATAACTTGAGT 3496
Db 63 AGGCTTTTCTTGGGATGATTTTCTAGTCTTAAGTTTGGGACATTAATAACTTGAGT 4
QY 3497 AC 3498
Db 3 AC 2

RESULT 3
US-09-016-434-680
; Sequence 680, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 680:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
```

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: HNT2NOT01
CLONE: 269891
US-09-016-434-680

Query Match 9.5%; Score 352.6; DB 4; Length 413;
Best Local Similarity 93.9%; Pred. No. 4.5e-82;
Matches 386; Conservative 0; Mismatches 23; Indels 2; Gaps 2;
QY 1022 GCGGAAATCAAAATTCATAAAATGAGG-CAAAAGGAGAAATGTGCCCCCAGGTCTCGAGGT 1080
Db 3 GCGGAAATCAAAATTCATAAAATGAGGAGAAATGTGCCCCCAGGTCTCGAGGT 62
QY 1081 CTGCATCACCATCAGGAAGGGGAAAGATTTCTGCAAAATGAGATAGCTGGCAGTCCG 1140
Db 63 CTGCATCACCATCAGGAAGGGGAAAGATTTCTGCAAAATGAGATAGCTGGCAGTCCG 122
QY 1141 TTCCACCCCTGCCAAGATGACTCCCTG-ACITCCAGGTAGAGTGAGGTTCAACAGC 1199
Db 123 TTCCANCCCTGCCAAGATGACGGGGGGAACCTCCANTTTTGAAGTGAGGTTCAACAGC 182
QY 1200 CTGTCCATCCCAAGCCACTAAGTCCAGATTCAGAGCTCCAGTCTTTCTGAAAGTTCTC 1259
Db 183 CTGTCCATCCCAAGCCACTAAGTCCAGATTCAGAGCTCCAGTCTTTCTGAAAGTTCTC 242
QY 1260 CTCCAAAGCAATGAAGAAGTTTCAGCACCTGCAAGAGAGACCTGCTGGAAATGTCAGA 1319
Db 243 CTCCAAAGCAATGAAGAAGTTTCAGCACCTGCAAGAGAGACCTGCTGGAAATGTCAGA 302
QY 1320 AGACAGTCTATCCAAATGGAGCGTCTCTTGCCCAACAGCAGGTGTTTCACATCAGTGTCT 1379
Db 303 AGACAGTCTATCCAAATGGAGCGTCTCTTGCCCAACAGCAGGTGTTTCACATCAGTGTCT 362
QY 1380 TCCGTGCTCTCTATTGCAACAAACAACTCAGTCTAGGAACATATGCATCTT 1430
Db 363 TCCGTGCTCTCTATTGCAACAAACAACTCAGTCTAGGAACATATGCATCTT 413

RESULT 4

US-09-016-434-493
Sequence 493, Application US/09016434
Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 493:

SEQUENCE CHARACTERISTICS:

LENGTH: 279 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: PROSNON01

CLONE: 2272243

US-09-016-434-493

Query Match

Best Local Similarity 99.6%; Pred. No. 1.3e-62;

Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2651 GCATAAGTGCTGTAAAGGCTTGAACCTGGGGAAATATTCACCTGATATAGCCCGAGATTC 2710
Db 1 GCGTAAGTGCTGTAAAGGCTTGAACCTGGGGAAATATTCACCTGATATAGCCCGAGATTC 60
QY 2711 TACTGTATTCCTCAAAAGCAATATTAAGGTAGATAGATGATTAGTAGTATATTGTTACAC 2770
Db 61 TACTGTATTCCTCAAAAGCAATATTAAGGTAGATAGATGATTAGTAGTATATTGTTACAC 120
QY 2771 ACTATTTTGGAAATTAGAGAAACATACAGAGGAATTTAGGGGCTTAAACATTACGACTGAA 2830
Db 121 ACTATTTTGGAAATTAGAGAAACATACAGAGGAATTTAGGGGCTTAAACATTACGACTGAA 180
QY 2831 TGCACCTTTAGTATATAAGGGGCACAGTTTCTATATTTTAAATGAATACCAATTTAAATTTT 2890
Db 181 TGCACCTTTAGTATATAAGGGGCACAGTTTCTATATTTTAAATGAATACCAATTTAAATTTT 240
QY 2891 TAGTATTTACCTGTTAAGAGATTATTTAGTCTTTAAATTT 2929
Db 241 TAGTATTTACCTGTTAAGAGATTATTTAGTCTTTAAATTT 279

RESULT 5

US-09-016-434-181

Sequence 181, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,434

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

```
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT09
; CLONE: 1422786
;
US-09-016-434-181

Query Match          6.0%; Score 224; DB 4; Length 238;
Best Local Similarity 98.3%; Pred. No. 9,149;
Matches 235; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 2114 GGAGAGACAGGAGAGAGAGTAAAGGAGTCTATAGTTTGGAGATGGAGATGAGAAATCTT 2173
Db 1 GGAGAGACAGGAGAGAGAGTAAAGGAGTCTATAGTTTGGAGATGGAGATGAGAAATCTT 60

QY 2174 GTAGAAAATGGTGCAGACTCCGATGAAGATGATAACAGCTTCTCTCAAAACAACATCTCCA 2233
Db 61 GTAGAAAATGGTGCAGACTCCGATGAAGATGATNACAGCTTCTCTCAAAACAACATCTCCA 120

QY 2234 CAAGAACCAAGTCTCTGAATTTGGTTCGAGTTTGTAGACAACACCTTTGCTGAAGAATTC 2293
Db 121 CAAGAACCAAGTCTCTGAATTTGGTTCGAGTTTGTAGACAACACCTTTGCTGAAGAATTC 180

QY 2294 ACTACTCAGAAATCAGAAATCCAGGATGTGAACTCTGGGAGGAGAGTGTGCAAGA 2352
Db 181 ACTACTCAGAAATCAGAAATCCAGGATGTGAA-TCCTGGGAGGAGAGTGTGCAAGA 238

RESULT 6
US-09-016-434-701
; Sequence 701, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
```

```
; INFORMATION FOR SEQ ID NO: 701:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 710 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HEARNOT01
; CLONE: 305403
;
US-09-016-434-701

Query Match          3.4%; Score 126.4; DB 4; Length 710;
Best Local Similarity 73.1%; Pred. No. 3,8e+23;
Matches 174; Conservative 1; Mismatches 62; Indels 1; Gaps 1;

QY 1313 TGTCAAGACAGTCTATCCAAATGGAGCGTCTCTTGGCCCAACAGCAGGTGTTTCACATC 1372
Db 24 TGTCAAGACAGTCTATCCAAATGGAGCGTCTCTTGGCCCAACAGCAGGTGTTTCACATC 83

QY 1373 AGCTGCTTCGGTCTCTCTATTGCAACAACAACACTCAGTCTAGG-AACATATGCATCTTT 1431
Db 84 TCCTGCTTCGGATGCCACCATTCGACAKATAAACTAAGTTTGGTAAATTTATCATCACT 143

QY 1432 ACATGGAAGATCTATTGTAAGCTCCTCAATCAACTCTTTAAATCTTAAGGCAACTA 1491
Db 144 TCATGCAAAATATCTGTAACCTCCTTTAAACAACTTTTCAAAATCCAAAGAAATTA 203

QY 1492 TGATGAAGGCTTTGGGCACAGACCACACAGAGGATCTATGGCAGCAAAATCAAAAC 1549
Db 204 TGATGAAGGCTTTGGACATTAAGCAGCATTAAGATGGAAGTCTGCAAAACCAAGC 261

RESULT 7
US-09-016-434-994
; Sequence 994, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 994:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 654 base pairs
; TYPE: nucleic acid
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Db 217 TAGGGTTTTTCATPAGGCTTGTTCGTTGCCACCATTCGAAGGGTACCCTCAAGCTTAG 276
QY 1417 AACATATGCACTTTTACATGGAAGAATCTATTGTAGCGCTCACTTCAATCAACTCTTTAA 1476
Db 277 CAACTACAACCTAATTTGAAGGGGTGCTATCTACGCGCCACACTATGATCAACTCTTCAA 336
QY 1477 ATCTAAGGGCAACTATCATGAAGGCTTTGGGCACAGCACCAACAAGGATCTATGGCGAAG 1536
Db 337 GAGAACTGGCGAGTCTTGACAGAAGTTTTTGAAGGAACACCAAGAGTTGTCAAACCTGAAG 396
QY 1537 CAAAAATGAAAACGA 1551
Db 397 ACAAAATCGATAGTA 411

RESULT 12
US-09-417-485D-5
; Sequence 5, Application US/09417485D
; Patent No. 6541202
; GENERAL INFORMATION:
; APPLICANT: Long, David M.
; APPLICANT: Metz, Anneke M.
; APPLICANT: Love, Ruschelle A.
; TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes
; FILE REFERENCE: 47714-5009-US
; CURRENT APPLICATION NUMBER: US/09/417,485D
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10640
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (834)..(7385)
; OTHER INFORMATION: TERT gene
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1821)..(1837)
; OTHER INFORMATION: m at position 1821 = a or c; w at position 1837 =
; OTHER INFORMATION: a or t. Xaa (amino acid) at position 330 = Leu or
; OTHER INFORMATION: Ile; Xaa at position 335 = Asp or Gly.
US-09-417-485D-5

Query Match 1.5%; Score 54.8; DB 4; Length 10640;
Best Local Similarity 47.9%; Pred. No. 0.0065;
Matches 224; Conservative 0; Mismatches 237; Indels 7; Gaps 2;
QY 2557 TTAAATCATAAACAACAAACAAAAACACAAAAACACATTCCTAAATCTAGAGTAAC 2616
Db 3763 TCAAAAAATAAAGTAAACAAAAATAACAATAACAAGAAAGAACAAAAATAATTATAACA 3822
QY 2617 TTACTTAAATCTTTCATTTTAGCAGTGATGATGTCATAGTGTGTAAGGCTTGTAACT 2676
Db 3823 ATAATAATTAATAATAACATAATAATAATAATAATAATAATAATAATAATAATAATA 3882
QY 2677 GGGGAAATATCCACCTGATTAATAGCCAGATTTCTACTGTATTCCTCAAAAGGCAATATTA 2736
Db 3883 ACAACAAATGTAAACTATCAAAATTCCTCAAAAGGTAATAATAAGAAATAATAATAATA 3942
QY 2737 AGGTAGATAGA-----TGATTAGTAGTATATTTGTTACACACTATTTTGGAAATTAGAGAAC 2791
Db 3943 AAAAGGCTAAAAATAATGAGAAGAACAAATATTGATGATTCCTCAATTTAGAAAAA 4002
QY 2792 ATACAGAAGGAATTTAGGGGCTTAAAC--ATTACGACTGATGCTTGTAGTATAAGGG 2849
Db 4003 AAAAAATATACATATATAAAAAATAAAAAATAATAATAAGAAAGAAATTTTATGTTAAAT 4062
QY 2850 CACAGTTTGTATATTTTAAATGAATACCAATTTTAAATTTTGTATTTTACCTGTTAAGA 2909
Db 4063 TAAATTCATCAATTTTATATCTAAAAGTTAAGAAATTAATGGATACCAAAAAA 4122

QY 2910 GATTATTAGTCTTTAAATTTTTTAGGTTAAATTTTCTTGCTGTATATATGAGGAATT 2969
Db 4123 AAGATTAAAGACCTTTTAAATTAATTTGTCTACTTTTAAATGTGCCAGAAATTTGCAAGCAAC 4182
QY 2970 TACTACTTTATGTCTCTCTCTAACTACATCTGAACTCGAACGCTCG 3017
Db 4183 CAATTTTGAATTTTGAAGAGTAAAAAAGCAGTGAATTTTATTTC 4230

RESULT 13
US-08-998-416-186/c
; Sequence 186, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtie, Philipp
; APPLICANT: Rebschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPIL
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 615 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1074RP
; US-08-998-416-186

Query Match 1.3%; Score 49.2; DB 3; Length 615;
Best Local Similarity 46.6%; Pred. No. 0.0042;
Matches 192; Conservative 0; Mismatches 218; Indels 2; Gaps 1;
QY 2571 AAAACAAAAACACAAAAACACATTCCTAAATCTAGAGTAACCTTTTACTTAAATCTT 2630
Db 511 AATAATAATAAAAAATTAATAATAAGTTAAATTAATTAATTAATTAATTAATTAAT 452
QY 2631 CATTTAGCAGTGATGATATGCATAAGTCTGTAGGCTTGTAACTGGGAAATATCCA 2690
Db 451 TATAAAAAGTTAAATAATTAATAATCAACATATATTTTATAAAAATAGATATATAATAA 392

QY	2691	CTGTATAATAGCCAGATTC	TCTCTGTATTCCCAAGGCAATATTAAGGTAGATAGTGA	2750
Db	391	AAATAAATTTACAATATTTAAATAAAATCTTTTAATAATAAAATATATTATT	--	334
QY	2751	TTAGTAGTATATTGTTACACACTATTTTGGAAATTTAGAGAACATACAGAGGAATTTAGGG	2810	
Db	333	TTAATAACAAATTAATAATAATATATTATTTATGATTAATCTATTTTAAATATTTATTA	274	
QY	2811	GCTTAAACATTACGACTGAAATGCACCTTTTAGTATAAAGGCGACAGTTTGTATATTTTAAA	2870	
Db	273	AGAAAAATAATAATATCTAATAATATTTTAACTAAATTTAAAAATTTGAACATAGACTAA	214	
QY	2871	TGAATACCAATTTAAATTTTTTTAGTATTTCCTGTTAAGAGATTATTTAGTCGTTTAAATTT	2930	
Db	213	ATAGTATTCATATAAATATTATTTTAAATTTATATAAATTAATTAATGATGAATTTAA	154	
QY	2931	TTTAGGTAAATTTCTTGCTGCGATATATATAGGGAATTTTACTACTTTATGT	2982	
Db	153	GTAATTTATATAATAATTTATATAAAGTATTAAATCAATAAATAAATTT	102	

RESULT 14

```

US-08-998-416-1137/c
; Sequence 1137, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippse, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgén
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:

```

	Query Match	1.3%	Score 48.4;	DB 3;	Length 636;
	Best Local Similarity	45.3%;	Pred. No. 0.0068;		
	Matches 214;	Conservative 0;	Mismatches 256;	Indels 2;	Gaps 1;
QY	2511	ATGAAATGTAAATTACTTGGACCTA	CTTTGGAAAAGAATTCCTCTT	AAAAATCAAACAAC	9570
Dd					
Dd	571	ATAAATTAATAAATTAATTTAAAT	TAAATAAATAAATAAATAAATAA	AAGTGAATATATATTTATTA	512
QY	2571	AAAACAAAAAAACACAAAAAACACAT	CTCTAAATACTAGAGATAACCTTT	ACTTTACTTAAATCTCT	2630
Dd					
Dd	511	AATAATATAAAAAATTAATAATAGA	AAATTAAGATTTAAATTTAAATTA	ATTAATTAATAATATCTCT	452
QY	2631	CATTTTAGCAGTGATGATATGCATA	AGTGCTGTAGGCTTTGAACCTGGG	CAATATTCOA	2690
Dd					
Dd	451	ATAAAAGAATTAATAATAATAATCA	CACATATTTATTAANAATAGATATT	TATATATAAA	392
QY	2591	CCTGATAATAGCCGAGTTCTACTGT	ATTTCCEAAAAGGCAATATTAAAG	TAGATAGTGA	2750
Dd					
Dd	391	AATAAATAATTACAAATATTTAATA	TAANTTAAATCTTTATAATAAATA	TATATTATT - -	334
QY	2751	TTAGTAGTATTTGTTACACACTATTT	TTCGAATTAGAGAACATACAGANG	AAGTAATTAGGG	2810
Dd					
Dd	333	TTAATAACAAATTAATAATAATATA	TATTAATTATTGATAATCTATTAA	TAAATTTATTAA	274
QY	2811	GCTTAACACATTACGACTGAATGCAC	TTTAGTATAAAGGCCACAGTTTGTA	TATTTTTTAAA	2870
Dd					
Dd	273	AGAAAATAATAATCTAATAATATT	TAACTAAITTAANAATTTGNACAT	AGACTAA	214
QY	2871	TGAATACCBAATTTAATTTTTTAGT	ATTATTAACCTGTTTAAGAGATTA	TTTAGTCTTTAAATTT	2930
Dd					
Dd	213	ATAGTATTCAATATAAATATTATTT	TATAATTTATATAAATTAATAAT	TATTAATGATGAATTA	154
QY	2931	TTTAGGTTAATTTCTTGCTGTGATAT	ATATAGGAAATTTACTACTTTATGT		2982
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US-09-601-198-55/c
; Sequence 55, Application US/09601198
; Patent No. 6531583
; GENERAL INFORMATION:
; APPLICANT: Cassell, Gail H.
; APPLICANT: Chen, Ellison Y.
; APPLICANT: Glass, Jennifer S.
; APPLICANT: Glass, John I.
; APPLICANT: Heiner, Cheryl R.
; APPLICANT: Lefkowitz, Elliot
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
; TITLE OF INVENTION: UREALYTICUM
; FILE REFERENCE: UAB-13452/22
; CURRENT APPLICATION NUMBER: US/09/601.198
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/073,189
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatenIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 3057
; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-55

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	Matches 99	Conservative 0	Mismatches 86	Indels 0	Gaps 0
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Db	634	AACCAATAAATTGATGATATCCGATTAATTAATTTGTAATGACCAATGGTAACCTAA	575		
QY	2621	TTAATCTCTTCATTTTAGCAGTGAATGATGCATAGTGTCTGAAGCCTTGTAACTGGG	2680		

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Db      514 AATTGTAAATTTGAAAATAAACCRAAATTCCTACCTATATAAAAAACATAAATAATGATTG 455
QY      2741 AGATA 2745
Db      454 AGATA 450
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Job time : 202 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2004, 09:57:07 ; Search time 1106 Seconds
(without alignments)

11594.961 Million cell updates/sec

Title: US-09-890-549-16

Perfect score:

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Scoring table: IDENTITY NIIC

Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Processing; Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA: *

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18: /cgn2_6/pdata/1/pubna/us60 PUBCOMB.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3568.8	96.3	3650	11	US-09-783-732-3	Sequence 3, Appli
2	3324.4	89.7	3543	11	US-09-783-733-1	Sequence 1, Appli
3	2797.6	75.5	2905	13	US-10-117-723-45	Sequence 45, Appli
4	2797.6	75.5	2905	15	US-10-037-270-45	Sequence 45, Appli
5	2736.4	73.9	2749	9	US-08-822-489A-399	Sequence 399, App
6	722	19.5	732	9	US-09-925-377-152	Sequence 152, App
7	500.6	15.9	698	15	US-10-198-846-10895	Sequence 10895, A
8	551	14.9	565	15	US-10-060-036-4338	Sequence 4338, Ap
9	548.8	14.8	583	15	US-10-066-543-3373	Sequence 3373, Ap
10	514.4	13.9	547	15	US-10-066-543-3300	Sequence 3200, Ap
11	383.2	10.3	404	11	US-09-918-995-7225	Sequence 7225, Ap
12	374.4	10.1	410	11	US-09-918-995-7296	Sequence 7296, Ap
C 13	362	9.8	565	11	US-09-871-161-139	Sequence 139, App
C 14	358	9.7	358	15	US-10-066-554-1533	Sequence 1533, Ap
C 15	279.8	7.6	283	10	US-09-998-598-1767	Sequence 1767, Ap

16	233	6.8	262	10	US-09-796-692-3900
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C 18	242	5.7	567	15	US-10-198-846-8531
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23	171.8	4.6	228	10	US-09-783-590-176
24	141.2	3.8	2379	9	US-09-880-192-13
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44	71.8	1.9	418	10	US-09-878-574-30
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ALIGNMENTS

RESULT 1

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US-09-783-732-3
; Sequence 3, Application US/09783732
; Publication NO. US20030054417A1
; GENERAL INFORMATION:
; APPLICANT: Chang, David D.
; APPLICANT: Maul, Raymond S.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: EPITHELIAL PROTEIN LOST IN NEOPLASM
; TITLE OF INVENTION: (EPIN)
; FILE REFERENCE: 10809/003001
; CURRENT APPLICATION NUMBER: US/09/783,732
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 09/668,400
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3650
; TYPE: DNA
; ORGANISM: Homosapien
US-09-783-732-3

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	Best Local Similarity	99.4%;	Pred. No. 0;		
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QY	104	TTTTAGCCAGGTATTTTCAGTGTCTGTAGACAGATGGGAATCATCTCCATTTAATAGACGG	163		
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QY	164	CAATGGACCTCACTATCATTTGAGGGTAAACAGCCAAAGAACATTTCTCTTGTCAAACAAGAC	223		
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RESULT 2

US-09-783-732-1
; Sequence 1, Application US/09783732
; Publication No. US20030054417A1
; GENERAL INFORMATION:
; APPLICANT: Chang, David D.
; APPLICANT: Maul, Raymond S.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: EPITHELIAL PROTEIN LOST IN NEOPLASM
; TITLE OF INVENTION: (EPLIN)
; FILE REFERENCE: 10809/003001
; CURRENT APPLICATION NUMBER: US/09/783,732
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 09/658,400
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Homosapien
US-09-783-732-1

Query Match 89.7%; Score 3324.4; DB 11; Length 3543;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3371; Conservative 0; Mismatches 11; Indels 10; Gaps 3;

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Db 159 AACACCGAAATCTCTCCAGCACCTTTAGAAAGGGAGCCCTGACTGTGTTAAAGAGAGAG 218
QY 362 TGGGAGAACCCAGGCTGGGAGCAGAGTCTCACAGACTCTCTACGGAACAGCAGCACT 421
Db 219 TGGGAGAACCCAGGCTGGGAGCAGAGTCTCACAGACTCTCTACGGAACAGCAGCACT 278
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Db 279 GAGATTAGGCACAGAGCAGACATCTCTCTGCTGAAGTGACAAGCCAGCTGCTTCTGGA 338
QY 482 GCCAAAGCTGACCAAGAGAACAAATCCACCCAGATCTAGACTCAGGTCACTTCTGAA 541
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QY 542 GCCCTCTGTTACGGTTCGATATCCCCACATCAAGGACGGTGAAGTCTTAAAGAGCACTCA 601
Db 399 GCCCTCTGTTACGGTTCGATATCCCCACATCAAGGACGGTGAAGTCTTAAAGAGCACTCA 458
QY 602 ACAGAAAGTAAAAAATGGAAAAATTTGCTAGGAGAAATCCAGGCAATGAAGTAGAAAAATCA 661
Db 459 ACAGAAAGTAAAAAATGGAAAAATTTGCTAGGAGAAATCCAGGCAATGAAGTAGAAAAATCA 518
QY 662 GAAATCAGTGAACACAGATGCTTCGGGCAAAATAGAGAAATATAATGTTCGCTGAAC 721
Db 519 GAAATCAGTGAACACAGATGCTTCGGGCAAAATAGAGAAATATAATGTTCGCTGAAC 578
QY 722 AGGCTTAAAGTATGTTTGAAGAGGTGAACCAACTCAAACTAGATTTCTCCGGCCCCAA 781
Db 579 AGGCTTAAAGTATGTTTGAAGAGGTGAACCAACTCAAACTAGATTTCTCCGGCCCCAA 638

QY 782 AGCCGAAGTGCAGTGAAGGAAGATCTCTGAAAAAGAGTATTTCTAGATGACCTGGAA 841
Db 639 AGCCGAAGTGCAGTGAAGGAAGATCTCTGAAAAAGAGTATTTCTAGATGACCTGGAA 698
QY 842 ATAGGCCAGGTGAGTGTGATCTCTAGATTTGACTCGGAGAAAAATCAGAGTAGACGA 901
Db 699 ATAGGCCAGGTGAGTGTGATCTCTAGATTTGACTCGGAGAAAAATCAGAGTAGACGA 758
QY 902 AATCTGGAATCTCCAGCCCTCTCAGAAACCTCTATAAAGGATCGAATGGCCCAAGTACCAG 961
Db 759 AATCTGGAATCTCCAGCCCTCTCAGAAACCTCTATAAAGGATCGAATGGCCCAAGTACCAG 818
QY 962 GCAGCTGTGTCAAAACAAAGAGAGCTCAACCAACTATACAAATGAGCTGAAAGCCAGTGT 1021
Db 819 GCAGCTGTGTCAAAACAAAGAGAGCTCAACCAACTATACAAATGAGCTGAAAGCCAGTGT 878
QY 1022 GGGGAATCAAAATTCATAAATGGAGCAAAAGGAAATGTGCCCCCAGGCTCTGAGGTC 1081
Db 879 GGGGAATCAAAATTCATAAATGGAGCAAAAGGAAATGTGCCCCCAGGCTCTGAGGTC 938
QY 1082 TGCATCACCCTCAGGAAGGGAAAAAGATTTCTGCAATGAGAATAGCCTGGCAGTCCGT 1141
Db 939 TGCATCACCCTCAGGAAGGGAAAAAGATTTCTGCAATGAGAATAGCCTGGCAGTCCGT 998
QY 1142 TCCACCCCTGCGGAAGATGACTCCC---GTGACTCCAGGTTAAGAGTAGGTTCAACAG 1198
Db 999 TCCACCCCTGCGGAAGATGACTCCCAGGTGACTCCCAGGTTAAGAGTAGGTTCAACAG 1058
QY 1199 CTTGTCCATCCCAAGCCAGTCTAGTCCAGATTCAGAGCCCTCAGTCTTTCTGAAAAGTCT 1258
Db 1059 CTTGTCCATCCCAAGCCAGTCTAGTCCAGATTCAGAGCCCTCAGTCTTTCTGAAAAGTCT 1118
QY 1259 CTTCCCAAGCAATGAAGAAGTTTCAGGCACCTGCAAGAGAGACCTGGTGGAAATGTGAG 1318
Db 1119 CTTCCCAAGCAATGAAGAAGTTTCAGGCACCTGCAAGAGAGACCTGGTGGAAATGTGAG 1178
QY 1319 AAGACAGTCTATCCAAATGAGGCTCTTTGGCAACAGCAGGTTTCAATCAGCTGC 1378
Db 1179 AAGACAGTCTATCCAAATGAGGCTCTTTGGCAACAGCAGGTTTCAATCAGCTGC 1238
QY 1379 TTCCGTTGCTCTATTGCAACCAACAACTCAGTCTAGNACATATGCAATCTTTACATGGA 1438
Db 1239 TTCCGTTGCTCTATTGCAACCAACAACTCAGTCTAGNACATATGCAATCTTTACATGGA 1298
QY 1439 AGAATCTATTGTAAGGCTCAGTCTCAATCAACTCTTTTAAATCTAAGGGCAACTATGATGAA 1498
Db 1299 AGAATCTATTGTAAGGCTCAGTCTCAATCAACTCTTTTAAATCTAAGGGCAACTATGATGAA 1358
QY 1499 GGTCTTGGCACAGACCAAGAGTCTATGGCAAGCAAAATGAAAAAGAGAGATT 1558
Db 1359 GGTCTTGGCACAGACCAAGAGTCTATGGCAAGCAAAATGAAAAAGAGAGATT 1418
QY 1559 TTGGAGAGACCCAGCTTGCAAATGCAAGGGAGACCCCTCAAGCCAGGGGTAGAA 1618
Db 1419 TTGGAGAGACCCAGCTTGCAAATGCAAGGGAGACCCCTCAAGCCAGGGGTAGAA 1478
QY 1619 GATGCCCTATTGCTAAGGTGGTGTCTGCTGCTGCAAGTATGGAGCCCAAGGCTCTCT 1678
Db 1479 AATGCCCTATTGCTAAGGTGGTGTCTGCTGCTGCAAGTATGGAGCCCAAGGCTCTCT 1538
QY 1679 CAGCAGGAGAGAGAACAGCCAGCTGAAACCAAGAGAGCTGAGGATCGCTGGCCACCC 1738
Db 1539 CAGCAGGAGAGAGAACAGCCAGCTGAAACCAAGAGAGCTGAGGATCGCTGGCCACCC 1598
QY 1739 CCCACTGAATTTGGAAGTTCAGAGAGTGCCTTGGAGGAGGATCAAAATGTCAAGGCC 1798
Db 1599 CCCACTGAATTTGGAAGTTCAGAGAGTGCCTTGGAGGAGGATCAAAATGTCAAGGCC 1658
QY 1799 AAATGGCTCTGTAAGAGCAATCAGAGCCCGAGTTCTCTGAGGATGTCATCTAGAT 1858
Db 1659 AAATGGCTCTGTAAGAGCAATCAGAGCCCGAGTTCTCTGAGGATGTCATCTAGAT 1718

QY 1859 CTGAAGAAGCTTAAGACGATCTTCTCACTGAAGAAAAAGAGCCGCCATTCTACCTGTAGCA 1918
Db 1719 CTGAAGAAGCTTAAGACGATCTTCTCACTGAAGAAAAAGAGCCGCCATTCTACCTGTAGCA 1778
QY 1919 GCTTCATTTCAAAGCACTCTGTCAAGAGCCAAAACTGTGTCTCCCACTCTACAGAAA 1978
Db 1779 GCTTCATTTCAAAGCACTCTGTCAAGAGCCAAAACTGTGTCTCCCACTCTACAGAAA 1838
QY 1979 GGCTGGAGCATGTGAGAGCAGAGTGAAGTCTGTGGTGGAGAGTTGAGAAAGAAA 2038
Db 1839 GGCTGGAGCATGTGAGAGCAGAGTGAAGTCTGTGGTGGAGAGTTGAGAAAGAAA 1898
QY 2039 CAAGTGGAAAAATGCAAGGCTTCTAAGAAATGGGAATGTGGAAAAAAACAACCTGGCAA 2098
Db 1899 CAAGTGGAAAAATGCAAGGCTTCTAAGAAATGGGAATGTGGAAAAAAACAACCTGGCAA 1958
QY 2099 AACAAAGATCTAAGAGAGACAGGGAAGAGTGAAGGAAGTCTAGTCTGGAGATG 2158
Db 1959 AACAAAGATTTAAAGAGAGACAGGGAAGAGTGAAGGAAGTCTAGTCTGGAGATG 2018
QY 2159 GAGATGAGATCTTGTAGAAATGGTGCAGACTCCCATGAAGATGATAACAGCTTCCCTC 2218
Db 2019 GAGATGAGATTTTGTAGAAATGGTGCAGACTCCCATGAAGATGATAACAGCTTCCCTC 2078
QY 2219 AAAACAACATCTCCACAAGAACCCAGTCTCTGAATTTGGTGGAGTTTGTAGACAACACC 2278
Db 2079 AAAACAACATTTCCACAAGAACCCAGTCTTGAATTTGGTGGAGTTTGTAGACAACACC 2138
QY 2279 TTTGCTGAAAGATTTCACTACTCAGAAATCCAGGATGTGAACTCTGGAGGGA 2338
Db 2139 TTTGCTGAAAGATTTCACTACTCAGAAATCCAGGATGTGAACTTTGGAGGGA 2198
QY 2339 GAAGTGTCAAAGAGCTCTCTGTGGAAAGACAGATAAAGAGAAATCGGTATTATGATGAG 2398
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QY 2399 GATGAGATGAAGAGTGCACAAATTCGAATGATCTGGCCCTTAAATTCATCTAGTGTGA 2458
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QY 2459 GCGAGCCACTGCCCTTTGTCAAAATGTGACACATAAGCAGGTATCCCAGCATGAAATG 2518
Db 2319 GCGAGCCACTGCCCTTTGTCAAAATGTGACACATAAGCAGGTATCCCAGCATGAAATG 2378
QY 2519 TAATTTACTTTGGAAGTAACTTTGGAAAAAGAAATTCCTTCTTAAATCAAAAAACAAAA 2578
Db 2379 TAATTTACTTTGGAAGTAACTTTGGAAAAAGAAATTCCTTCTTAAATCAAAAAACAAAA 2438
QY 2579 AAAACACAAAAACACATTTCTAAATACTAGAGATAAATCTTAAATCTTCAATTTAG 2638
Db 2439 AAAACACAAAAACACATTTCTAAATACTAGAGATAAATCTTAAATCTTCAATTTAG 2598
QY 2639 CAGTGATGATATGCATAAGTGTGTAAGGCTTGTAACTGGGAAATATCCACCTGATA 2698
Db 2494 CAGTGATGATATGCATAAGTGTGTAAGGCTTGTAACTGGGAAATATCCACCTGATA 2553
QY 2699 TAGCCAGATTTCTACTGATTTCCAAAAAGGCAATATTAAGGTAGATAGATGATTAGT 2758
Db 2554 TAGCCAGATTTCTACTGATTTCCAAAAAGGCAATATTAAGGTAGATAGATGATTAGT 2613
QY 2759 ATATTGTACACACTATTTTGGAAATTAGAGAACATACAGAGGAATTTAGGGCTTTAAAC 2818
Db 2614 ATATTGTACACACTATTTTGGAAATTAGAGAACATACAGAGGAATTTAGGGCTTTAAAC 2673
QY 2819 ATTACACATGAATGCACTTTAGTATAAAGGGCAGCTTTGTATATTTTAAATGAATACC 2878
Db 2674 ATTACACATGAATGCACTTTAGTATAAAGGGCAGCTTTGTATATTTTAAATGAATACC 2733
QY 2879 AATTTAATTTTTTAGTATTTTACCTGTTAAGAGATATTTTAGTCTTTTAAATTTTTTAGGTT 2938
Db 2734 AATTTAATTTTTTAGTATTTTACCTGTTAAGAGATATTTTAGTCTTTTAAATTTTTTAGGTT 2793
QY 2939 AATTTCTTGTGTGATATATATGAGGAATTTTACTATTTATGCTCTCTCTAAACTA 2998

Db 2794 AATTTCTTGTGATATATAGGAATTTACTACTTTATGTCCTCTCTCTAAACTA 2853
Qy 2999 CATCTGAACCTCGAGCTCTCGAGGTATATACACAGAGCACTTTTGGAGCAATGAAA 3058
Db 2854 CATCTGAACCTCGAGCTCTCGAGGTATATACACAGAGCACTTTTGGAGCAATGAAA 2911
Qy 3059 AACCAACCTACACTCTTCGGTGCTTAGAGAGATCTGCTCTCCAAATAAGCTTTTGTA 3118
Db 2912 AACCAACCTACACTCTTCGGTGCTTAGAGAGATCTGCTCTCCAAATAAGCTTTTGTA 2971
Qy 3119 TCTGCCAGTGAATTTACTGTACTCCAAATGATGCTTTCTTTCTGCTGATATCTGTGCT 3178
Db 2972 TCTGCCAGTGAATTTACTGTACTCCAAATGATGCTTTCTTTCTGCTGATATCTGTGCT 3031
Qy 3179 TCTCATATTTACTGAAAGCTCGAATATTTTAGTAATACCTTTCCGGATCACTGTCCCCAT 3238
Db 3032 TCTCATATTTACTGAAAGCTCGAATATTTTAGTAATACCTTTCCGGATCACTGTCCCCAT 3091
Qy 3239 CTTCGGTGTAGAGCAAGTCAAGAGTTTAAAGGAGGAAGAAAGCACTGTCTTACAC 3298
Db 3092 CTTCGGTGTAGAGCAAGTCAAGAGTTTAAAGGAGGAAGAAAGCACTGTCTTACAC 3151
Qy 3299 CACTTGAGCTCAGACCTCTAAACCTGTATTTCCCTTATGATGTCCTCTTTTGGAGAC 3358
Db 3152 CACTTGAGCTCAGACCTCTAAACCTGTATTTCCCTTATGATGTCCTCTTTTGGAGAC 3211
Qy 3359 TAAATTTTAAATCTACTAGCTCTGAAATATATATGATTTTATCAAGTATTTCTCAGG 3418
Db 3212 TAAATTTTAAATCTACTAGCTCTGAAATATATATGATTTTATCAAGTATTTCTCAGG 3271
Qy 3419 TGAATTTAAACCACTATAGGCTTTTCTTGGATGATTTTCTAGTCTTAAAGTTTGGG 3478
Db 3272 TGAATTTAAACCACTATAGGCTTTTCTTGGATGATTTTCTAGTCTTAAAGTTTGGG 3331
Qy 3479 GACATTTAAACCTTGAAGTACATTTGTTGTACACAGTTGATTTCCAAATTTGATGGATGG 3538
Db 3332 GACATTTAAACCTTGAAGTACATTTGTTGTACACAGTTGATTTCCAAATTTGATGGATGG 3391
Qy 3539 GAGGAGAGGTGCTTAAAGCTGTAGGCTTTTCTTTGACTGCAATTTATAGAGATTTAGCT 3598
Db 3392 GAGGAGAGGTGCTTAAAGCTGTAGGCTTTTCTTTGACTGCAATTTATAGAGATTTAGCT 3451
Qy 3599 TTAATATTTTAAAGATGTAAACATTTCTTCTTCTAGTCTTACCTAGTCTGAAACAT 3658
Db 3452 TTAATATTTTAAAGATGTAAACATTTCTTCTTCTAGTCTTACCTAGTCTGAAACAT 3511
Qy 3659 TTTTATTTCAATAAGATTTTAAATTTAAATTTG 3690
Db 3512 TTTTATTTCAATAAGATTTTAAATTTAAATTTG 3543

RESULT 3

US-10-117-722-45
; Sequence 45, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Dmanac, Radjoje T.
; TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2BCIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: Pf_genes Version 1.0
; SEQ ID NO 45
; LENGTH: 2905
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (173) .. (2452)
US-10-117-722-45

Query Match 75.5%; Score 2797.6; DB 13; Length 2905;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2842; Conservative 0; Mismatches 24; Indels 10; Gaps 2;

Qy 4 CGCAGGAGCAGTAGGTGTTAGCAGCTTGTGCGACAGGTGCGTAGGTAGGAGCGCCGG 63
Db 40 CCGGGTCACGATTTCTGAGCAGCTTGTGCGACAGGTGCGTAGGTAGGAGCGCCGG 99
Qy 64 ACTGTGACAGGGCTGTTAGCAGCGCAGAGGAAAGCGGCTTTTACCCAGGTATTTCACT 123
Db 100 ACCTGTGACAGGGCTGTTAGCAGCGCAGAGGAAAGCGGCTTTTACCCAGGTATTTCACT 159
Qy 124 GTCTGTAGACAAGATGGAATCATCTCCATTTTATAGACGGCAATGGACCTCACTATCAT 183
Db 160 GTCTGTAGACAAGATGGAATCATCTCCATTTTATAGACGGCAATGGACCTCACTATCAT 219
Qy 184 GAGGTTAACAGCAAGAACTTTCTCTGTCACAGAACAAAGTATCGGCTATTTGTGGA 243
Db 220 GAGGTTAACAGCAAGAACTTTCTCTGTCACAGAACAAAGTATCGGCTATTTGTGGA 279
Qy 244 AATATTTCTCAAGTACCAGAAAGCAGCTGAAAGAAACAAACATGGAGAAAGAGAGTAA 303
Db 280 AATATTTCTCAAGTACCAGAAAGCAGCTGAAAGAAACAAACATGGAGAAAGAGAGTAA 339
Qy 304 CACCGAAATTTCTCTCCAGCATTTTAGAAAGGGGACCTGACTGTGTTAAAGAAAGAGTG 363
Db 340 CACCGAAATTTCTCTCCAGCATTTTAGAAAGGGGACCTGACTGTGTTAAAGAAAGAGTG 399
Qy 364 GGAGAACCCAGGGCTGGGAGCAGAGTCTCACACAGCTCTCTACGGAACAGCAGCACTGA 423
Db 400 GGAGAACCCAGGGCTGGGAGCAGAGTCTCACACAGCTCTCTACGGAACAGCAGCACTGA 459
Qy 424 GATTAGGCACAGCAGACCACTCTCTGCTGAGGTGACAGCTCTAGACTCAGCTCCTCTGGAGC 483
Db 460 GATTAGGCACAGCAGACCACTCTCTGCTGAGGTGACAGCTCTAGACTCAGCTCCTCTGGAGC 519
Qy 484 CAAAGCTGACCAAGAAAGCAAAATCCACCCAGATCTTAGACTCAGCTCCTCTGAAAGC 543
Db 520 CAAAGCTGACCAAGAAAGCAAAATCCACCCAGATCTTAGACTCAGCTCCTCTGAAAGC 579
Qy 544 CCTCTTCAGGGTCGATATCCACATCAAGGACGGTGAGGATCTTAAAGACCACTCAAC 603
Db 580 CCTCTTCAGGGTCGATATCCACATCAAGGACGGTGAGGATCTTAAAGACCACTCAAC 639
Qy 604 AGAAGTAAAGAAATGGAAGAAATTTGCTAGGAGATCCAGGATGAAGTAGAAAAATCAGA 663
Db 640 AGAAGTAAAGAAATGGAAGAAATTTGCTAGGAGATCCAGGATGAAGTAGAAAAATCAGA 699
Qy 664 AATCAGTGAAGAAACAGATGCTTCGGGCAAAATAGAGAAATATATGTTCCGCTGAAACAG 723
Db 700 AATCAGTGAAGAAACAGATGCTTCGGGCAAAATAGAGAAATATATGTTCCGCTGAAACAG 759
Qy 724 GCTTAAGATGATGTTTGAAGAAAGTGAAACCACTCAAACTAAGATTTCTCCGGGCCCAAG 783
Db 760 GCTTAAGATGATGTTTGAAGAAAGTGAAACCACTCAAACTAAGATTTCTCCGGGCCCAAG 819
Qy 784 CCGAAGTGAAGTGAAGAAAGATCTCTGAAAAACAGCTATTTCTCTAGATGACCTGGAAT 843
Db 820 CCGAAGTGAAGTGAAGAAAGATCTCTGAAAAACAGCTATTTCTCTAGATGACCTGGAAT 879
Qy 844 AGGCCAGGTGAGTTGTCATCTTCTACATTTGACTCCGAGAAAAATAGAGTAGACAAAA 903

Db	880	AGGCCCAGGTCAGTTGTTTCATCTCTTACATTTTGAATCGGAGAAAAATGAGAGTAGACGAAA	933
Qy	904	TCCTGGAACCTTCACGCCCTCTCAGAAACCTCTATAAAGGATCGAATGCGCAGTACACAGGC	963
Db	940	TCGTGAACTTTCACGCCCTCTCAGAAACCTCTATAAAGGATCGAATGCGCAGTACACAGGC	999
Qy	964	AGCTGTGTCCAAACAAAGCAGCTCAACCAACTATACAAATGAGCTGAAAGCCAGCTGGTGG	1023
Db	1000	AGCTGTGTCCAAACAAAGCAGCTCAACCAACTATACAAATGAGCTGAAAGCCAGCTGGTGG	1059
Qy	1024	CGAAATCAAAATTCATAAAATGGAGCAAAAGAGAAATGTGCCGCCAGGTCTCTGAGGCTCG	1083
Db	1060	CGAAATCAAAATTCATAAAATGGAGCAAAAGAGAAATGTGCCGCCAGGTCTCTGAGGCTCG	1119
Qy	1084	CATCACCCATCAGGAAGGGGAAAGATTCTGCAAAATGAGAAATAGCTGGCAGTCCGCTTC	1143
Db	1120	CATCACCCATCAGGAAGGGGAAAGATTCTGCAAAATGAGAAATAGCTGGCAGTCCGCTTC	1179
Qy	1144	CACCCCTCGGAAGATGACTCCCGTGACTCCCAAGTTAAGAGTGAGGTTCAACAGACCTGT	1203
Db	1180	CACCCCTCGGAAGATGACTCCCGTGACTCCCAAGTTAAGAGTGAGGTTCAACAGACCTGT	1239
Qy	1204	CCATCCCAGACCACTAAGTCCAGATTCCAGAGCTCCAGTCTTTCTGAAAGTCTTCCTCC	1263
Db	1240	CCATCCCAGACCACTAAGTCCAGATTCCAGAGCTCCAGTCTTTCTGAAAGTCTTCCTCC	1299
Qy	1264	CAAAAGCAATGAAGAAGTTTCAGGCACCTGCAAGAGAGACCTGCGTGGAAATGTCAGAGAC	1323
Db	1300	CAAGCAATGAAGAAGTTTCAGGCACCTGCAAGAGAGACCTGCGTGGAAATGTCAGAGAC	1359
Qy	1324	AGTCTATCCAAATGAGAGCGTCTCTTGGCCAAACAGCAGGTTTTCACATCAGCTGCTTCCG	1383
Db	1360	AGTCTATCCAAATGAGAGCGTCTCTTGGCCAAACAGCAGGTTTTCACATCAGCTGCTTCCG	1419
Qy	1384	TGCTCTCTATTGCAACCAACCAACTCAGCTAGGAAACATATGCATCTTTATGGAAGAAT	1443
Db	1420	TGCTCTCTATTGCAACCAACCAACTCAGCTAGGAAACATATGCATCTTTATGGAAGAAT	1479
Qy	1444	CTATTGTAAGCCTCACTTCAATCAACTCTTTAAATCTAAGGCAACTATCATCAAGGCTT	1503
Db	1480	CTATTGTAAGCCTCACTTCAATCAACTCTTTAAATCTAAGGCAACTATCATCAAGGCTT	1539
Qy	1504	TGGGCACAGACCAACAAGGATCTATGGGCAAGCAAAAATGAAAACGAAGAGATTTTGA	1563
Db	1540	TGGGCACAGACCAACAAGGATCTATGGGCAAGCAAAAATGAAAACGAAGAGATTTTGA	1599
Qy	1564	GAGACCAAGCCAGCTTGCATGCAAGGAGACCCCTCAGAGCCGAGGGTGAAGATGC	1623
Db	1600	GAGACCAAGCCAGCTTGCATGCAAGGAGACCCCTCAGAGCCGAGGGTGAAGATGC	1659
Qy	1624	CCCTATTGCTAAGTGGGTGTCTGGCTGCAAGTATGGAAGCAAGGCTCTCTCTCAGCA	1683
Db	1660	CCCTATTGCTAAGTGGGTGTCTGGCTGCAAGTATGGAAGCAAGGCTCTCTCTCAGCA	1719
Qy	1684	GGAGAACGAAGACAGGCCAGCTGAAACCAAGAGAGCTGAGGATCGCTGGCCACCCCCCAC	1743
Db	1720	GGAGAACGAAGACAGGCCAGCTGAAACCAAGAGAGCTGAGGATCGCTGGCCACCCCCCAC	1779
Qy	1744	TGAACCTGGAAAGTTTCAGAAAGTCCCTTGGAGGAGGATCAAAATGTCAAAGCCCAATG	1803
Db	1780	TGAACCTGGAAAGTTTCAGAAAGTCCCTTGGAGGAGGATCAAAATGTCAAAGCCCAATG	1839
Qy	1804	GCCTCTGGAAGCAAAATCAGCAAGCCGCAAGTTCTCTGAGGATGTCATCTAGATCTGAA	1863
Db	1840	GCCTCTGGAAGCAAAATCAGCAAGCCGCAAGTTCTCTGAGGATGTCATCTAGATCTGAA	1899
Qy	1864	GAAGCTTAAGACGATCTCTTCACTGAAGGAAAGAGCCGCCCAATCTACTGTAGCAGCTTC	1923
Db	1900	GAAGCTTAAGACGATCTCTTCACTGAAGGAAAGAGCCGCCCAATCTACTGTAGCAGCTTC	1959
Qy	1924	ATTTCAAAGCACTCTGTCAAGAGCCCAAAATCTGTCTCCCACTATCAGAAAGGCTG	1983
Db	1960	ATTTCAAAGCACTCTGTCAAGAGCCCAAAATCTGTCTCCCACTATCAGAAAGGCTG	2019

RESULT 4

REF ID: A66014
US-10-037-270-45

Sequence 45, Application US/10037270

Publication No. US20030104529A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie
APPLICANT: Pen Feiwan

APPLICANT: Ren, Felyan

THE UNIVERSITY OF CHICAGO

APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yionghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yuning
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt FL_genes Version 1.0
SEQ ID NO 45_
LENGTH: 2905
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (173)..(2452)
US-10-037-270-45

Query Match 75.5%; Score 2797.6; DB 15; Length 2905;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2842; Conservative 0; Mismatches 24; Indels 10; Gaps 2;
QY 4 CGCAGGAGCAGTAGGTGTTAGCAGCTTGGTCGGACAGGTGCGCTAGGTAGAGCGCGGG 63
DB 40 CCGGGTCGACGATTCCTAGCAGCTTGGTCGGACAGGTGCGCTAGGTAGAGCGCGGG 99
QY 64 ACCTGTACAGGGGTGTAGCAGCGCAGAGAAAGGCGGCTTTAGCCAGGTATTCAGT 123
DB 100 ACCTGTACAGGGGTGTAGCAGCGCAGAGAAAGGCGGCTTTAGCCAGGTATTCAGT 159
QY 124 GTCTGTAGACAAGTGAATCATCTCCATTTAATAGAGGCGCATGACCTCAGTATCAT 183
DB 160 GTCTGTAGACAAGTGAATCATCTCCATTTAATAGAGGCGCATGACCTCAGTATCAT 219
QY 184 GAGGTTAACAGCCAAAGAACTTTCTCTGTCAACAAGAACTCATCGGCTATGTGGA 243
DB 220 GAGGTTAACAGCCAAAGAACTTTCTCTGTCAACAAGAACTCATCGGCTATGTGGA 279
QY 244 AATATTTCCAAAGTACAGAAAGCAGCTGAAGAAACAAACATGGAGAAAGAGAGTAA 303
DB 280 AATATTTCCAAAGTACAGAAAGCAGCTGAAGAAACAAACATGGAGAAAGAGTAA 339
QY 304 CACGAAATCTCTCCAGCAGCTTTAGAAAGGAGCCCTGACTGTGTTAAAGAAAGTG 363
DB 340 CACGAAATCTCTCCAGCAGCTTTAGAAAGGAGCCCTGACTGTGTTAAAGAAAGTG 399
QY 364 GGAGAACCCAGGGCTGGAGCAGAGTCTCACACAGACTCTCTACGGAACAGCAGACTCA 423
DB 400 GGAGAACCCAGGGCTGGAGCAGAGTCTCACACAGACTCTCTACGGAACAGCAGACTCA 459
QY 424 GATTAGGCACAGAGCAGACCATCTCTCTGCTGAAGTGACAAGCCAGCTGCTTCTGGAGC 483
DB 460 GATTAGGCACAGAGCAGACCATCTCTCTGCTGAAGTGACAAGCCAGCTGCTTCTGGAGC 519
QY 484 CAAAGTGCACCAAGAGACAAATCCACCCAGATCTTAGACTCAGGTCACTCTCTGAAGC 543
DB 520 CAAAGTGCACCAAGAGACAAATCCACCCAGATCTTAGACTCAGGTCACTCTCTGAAGC 579
QY 544 CTTCTGTTAGGGTCGATATCCCCACATCAAGACGCTGAGGATCTTAAGACCATCTCAAC 603
DB |||||

DB 580 CCTCGTTAGGGTCGATATCCCCACATCAAGGACGGTGAGGATCTTTAAAGACCACCTCAAC 639
QY 604 AGAAAGTAAAAAATGGAAAAATTTGCTAGAGAAATCCAGGCATGAAGTAGAAAAATCAGA 663
DB 640 AGAAAGTAAAAAATGGAAAAATTTGCTAGAGAAATCCAGGCATGAAGTAGAAAAATCAGA 699
QY 664 AATCAGTGAAAAACACAGATGCTTCGGGCAAAATAGAGAAATATAATGTTCCCGCTGAACAG 723
DB 700 AATCAGTGAAAAACACAGATGCTTCGGGCAAAATAGAGAAATATAATGTTCCCGCTGAACAG 759
QY 724 GCTTAAGATGATGTTTTGAGAAAGGTGAACCAACTCAAACTAAGATTCTCCGGGCCCAAG 783
DB 760 GCTTAAGATGATGTTTTGAGAAAGGTGAACCAACTCAAACTAAGATTCTCCGGGCCCAAG 819
QY 784 CGAAGTGCAAGTGAAGGAAGATCTCTGAAACAGCTATTCTCTAGATGACCTGGAAT 843
DB 820 CGAAGTGCAAGTGAAGGAAGATCTCTGAAACAGCTATTCTCTAGATGACCTGGAAT 879
QY 844 AGSCCCAGGTGCTGCTCATCTCTACATTTGACTCGGAGAAAAATGAGAGTAGAGAAA 903
DB 880 AGSCCCAGGTGCTGCTCATCTCTACATTTGACTCGGAGAAAAATGAGAGTAGAGAAA 939
QY 904 TCTGGAACCTCCAGGCTCTCAGAAACCTCTATAAAGGATCGAATGGCCCAAGTACCAGC 963
DB 940 TCTGGAACCTCCAGGCTCTCAGAAACCTCTATAAAGGATCGAATGGCCCAAGTACCAGC 999
QY 964 AGCTGTGTCCTCAAAACAAAGCAGCTCAACCAACTATACAAATGAGCTGAAAGCCAGTGTG 1023
DB 1000 AGCTGTGTCCTCAAAACAAAGCAGCTCAACCAACTATACAAATGAGCTGAAAGCCAGTGTG 1059
QY 1024 CGAAATCAAAATTCATAAAATGGAGCAAAAGAGAAATGTGCCCCCAGGTCTCGAGGTCTG 1083
DB 1060 CGAAATCAAAATTCATAAAATGGAGCAAAAGAGAAATGTGCCCCCAGGTCTCGAGGTCTG 1119
QY 1084 CATCACCATCAGGAAGGGGAAAAAGATTCTGCAAAATGAGAAATAGCCTGGCAGTCCGTT 1143
DB 1120 CATCACCATCAGGAAGGGGAAAAAGATTCTGCAAAATGAGAAATAGCCTGGCAGTCCGTT 1179
QY 1144 CACCCCTCCGCAAGATGACTCCCGTGACTCCAGGTTAAGAGTGAAGTTCAACAGCTGT 1203
DB 1180 CACCCCTCCGCAAGATGACTCCCGTGACTCCAGGTTAAGAGTGAAGTTCAACAGCTGT 1239
QY 1204 CCATCCCAAGCCATTAAGTCCAGATTCCAGAGCCTCCAGTCTTTCTGAAAGTTCTCTCC 1263
DB 1240 CCATCCCAAGCCATTAAGTCCAGATTCCAGAGCCTCCAGTCTTTCTGAAAGTTCTCTCC 1299
QY 1264 CAAAGCAATGAAGAAGTTTTCAGGCACCTGCAAGAGAGACCTGCGTGGAAATGTCAAGAC 1323
DB 1300 CAAAGCAATGAAGAAGTTTTCAGGCACCTGCAAGAGAGACCTGCGTGGAAATGTCAAGAC 1359
QY 1324 AGTCTATCCAAATGGAGCGTCTTTGGCCCAACAGCAGGTGTTTCAATCAGCTGCTCCG 1383
DB 1360 AGTCTATCCAAATGGAGCGTCTTTGGCCCAACAGCAGGTGTTTCAATCAGCTGCTCCG 1419
QY 1384 TTGCTCTCTATTGCAACAAACAACTCAGTCTAGGAACATATGCATCTTTTACATGGAAGAT 1443
DB 1420 TTGCTCTCTATTGCAACAAACAACTCAGTCTAGGAACATATGCATCTTTTACATGGAAGAT 1479
QY 1444 CTAITGTAAGCCTCACTTCAATCAACTCTTTAAATCTTAAGGGCAACTATGATGAAGGCTT 1503
DB 1480 CTAITGTAAGCCTCACTTCAATCAACTCTTTAAATCTTAAGGGCAACTATGATGAAGGCTT 1539
QY 1504 TGGGCACAGACCAACAAGGATCTATGGGCAAGCAAAATGAAACCAAGAGATTTTGA 1563
DB 1540 TGGGCACAGACCAACAAGGATCTATGGGCAAGCAAAATGAAACCAAGAGATTTTGA 1599
QY 1564 GAGACCAAGCCAGCTTCAATGCAAGGGAGACCCCTCAGAGCCAGGGGTAGAAGATGC 1623
DB 1600 GAGACCAAGCCAGCTTCAATGCAAGGGAGACCCCTCAGAGCCAGGGGTAGAAGATGC 1659
QY 1624 CCCTATTGCTAAGGTGGGTGCTCTGGCTGCAAGTATGGAAGCCAAAGCCCTCTCTCAGCA 1683
DB 1660 CCCTATTGCTAAGGTGGGTGCTCTGGCTGCAAGTATGGAAGCCAAAGCCCTCTCTCAGCA 1719

QY 1684 GGAGAGGAGAGCAAGCCAGCTGAAACCAAGAGCTGAGATCGCTGGCCACCCCCAC 1743
Db 1720 GGAAGAGGAGAGCAAGCCAGCTGAAACCAAGAGCTGAGATCGCTGGCCACCCCCAC 1779
QY 1744 TGAACCTGGAAGTTGAGAGGTCCTTGGAGGAGGATCAAAATGTCAAAGCCCAATG 1803
Db 1780 TGAACCTGGAAGTTGAGAGGTCCTTGGAGGAGGATCAAAATGTCAAAGCCCAATG 1839
QY 1804 GCTCTCTGAAGAGGAAATCAGCAAGCCCGAAGTTCTGAGGATGTCGATCTAGATCTGAA 1863
Db 1840 GCTCTCTGAAGAGGAAATCAGCAAGCCCGAAGTTCTGAGGATGTCGATCTAGATCTGAA 1899
QY 1864 GAAGCTTAAGACGATCTTCTCACTGAAGCAAGAGCCGCCCATTCAGTGTAGAGCTTC 1923
Db 1900 GAAGCTTAAGACGATCTTCTCACTGAAGCAAGAGCCGCCCATTCAGTGTAGAGCTTC 1959
QY 1924 ATTTCAAAGCACCTCTGTCAAGAGCCCAAAATCTGTCCCCACCTATCAGAAAGGCTG 1983
Db 1960 ATTTCAAAGCACCTCTGTCAAGAGCCCAAAATCTGTCCCCACCTATCAGAAAGGCTG 2019
QY 1984 GAGCATGTGAGAGGAGGTGAAGAGTCTGTGGTGGAGAGTTGAGAAAGGAAACAAAGT 2043
Db 2020 GAGCATGTGAGAGGAGGTGAAGAGTCTGTGGTGGAGAGTTGAGAAAGGAAACAAAGT 2079
QY 2044 GGAATATGCCAAGGCTTCTAAGAAAGATGGGAATGTGGGAAACCACTGGCAAAACAA 2103
Db 2080 GGAATATGCCAAGGCTTCTAAGAAAGATGGGAATGTGGGAAACCACTGGCAAAACAA 2139
QY 2104 AGAATCTAAAGGAGAGACAGGAGGAGAGTGAAGAGTCAATGTGAGAGTGGAGAG 2163
Db 2140 AGAATCTAAAGGAGAGACAGGAGGAGAGTGAAGAGTCAATGTGAGAGTGGAGAG 2199
QY 2164 TGAGAAATCTTTAGAAAATGGTGCAGACTCCGATGAAGATGAACAGCTTCTCTCAACA 2223
Db 2200 TGAGAAATCTTTAGAAAATGGTGCAGACTCCGATGAAGATGAACAGCTTCTCTCAACA 2259
QY 2224 ACAATCTCCACAGAACCCCAAGTCTCTGAATGTGTCGAGTTTGTGAGACACACTTTGC 2283
Db 2260 ACAATCTCCACAGAACCCCAAGTCTCTGAATGTGTCGAGTTTGTGAGACACACTTTGC 2319
QY 2284 TGAAGAAATTCAGTCTCAGATCAAAATCCCAGGATGTGAACTCTGGGAGGAGAGT 2343
Db 2320 TGAAGAAATTCAGTCTCAGATCAAAATCCCAGGATGTGAACTCTGGGAGGAGAGT 2379
QY 2344 GGTCAAGAGCTCTCTGTGGAAGAACAGATAAAGAGAAATCGGTATTATGATGAGGATGA 2403
Db 2380 GGTCAAGAGCTCTCTGTGGAAGAACACATAAAGAGAAATCGGTATTATGATGAGGATGA 2439
QY 2404 GGATGAAGAGTGACAAATTTGCAATGATCCTGGGCTTTAAATTCATGTTAGTGTAGCGAG 2463
Db 2440 GGATGAAGAGTGACAAATTTGCAATGATCCTGGGCTTTAAATTCATGTTAGTGTAGCGAG 2499
QY 2464 CCACTGGCCCTTTGTCAAAATGTGATGCACATAAGCAGGTATCCCAGCATGAAATGTAAAT 2523
Db 2500 CCACTGGCCCTTTGTCAAAATGTGATGCACATAAGCAGGTATCCCAGCATGAAATGTAAAT 2559
QY 2524 TACTTGAAGTAACCTTTGGAAAAGAAATCCCTTCTTAAATCAAAACCAAAACAAACAA 2583
Db 2560 TACTTGAAGTAACCTTTGGAAAAGAAATCCCTTCTTAAATCAAAACCAAAACAAACAA 2612
QY 2584 ACAAAAAACACATCTTAATTAAGATAACTTTACTTAAATTTCTTAAATTTAGCAGTG 2643
Db 2613 --AAAAAACACATCTTAATTAAGATAACTTTACTTAAATTTCTTAAATTTAGCAGTG 2670
QY 2644 ATGATATGCAATAGTGTGTAGGCTTTGTAACCTGGGAAATATTTCCACCTGATAATAGCC 2703
Db 2671 ATGATATGCAATAGTGTGTAGGCTTTGTAACCTGGGAAATATTTCCACCTGATAATAG-C 2729
QY 2704 CAGATTTCTACTGTATTTCCCAAAAGGCAATATTAAAGGTAGATAGATTAGTAGTATATT 2763
Db 2730 CTTTTTTTCTTTATTTCCCATATGGCAATATTAAAGGTAGACAGATGATTAGTAGTATATT 2789

QY 2764 GTTACACACTATTTTGGAAATTAGAGAACATACAGAGAAATTTAGGGCTTTAAACATTAC 2823
Db 2790 GTTACACACTATTTTGGAAATTAGAGATCATACAGAGGATTTTAGGGCTTTAAACATTAC 2849
QY 2824 GACTGAATGCACCTTTAGTATAAAGGGCACAGTTTGTATATTTTAAATGAATACCA 2879
Db 2850 GACTGAATGCACCTTTAGTATAAAGGGCACAGTTTGTATATTTTAAATGAATACCA 2905

RESULT 5
US-09-822-849A-399
; Sequence 399, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403
; CURRENT APPLICATION NUMBER: US/09/822,849A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 399
; LENGTH: 2749
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-849A-399

Query Match 73.9%; Score 2736.4; DB 9; Length 2749;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2748; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 941 GATCGAATGCCAAGTACCAGGAGCTGTGTCCAAACAAAGCAGCTCAACCAACTATACA 1000
Db 1 GATCGAATGCCAAGTACCAGGAGCTGTGTCCAAACAAAGCAGC.CAACCAACTATACA 60
QY 1001 AATGAGCTGAAAGCCAGTGGTGGGAAATCAAAATTCATAAAATGAGCAAAAGAGAAAT 1060
Db 61 AATGAGCTGAAAGCCAGTGGTGGGAAATCAAAATTCATAAAATGAGC-AAAGGAGAAAT 119
QY 1061 GTGCCCCCAGGTCCTGAGGTCTGCATCAGGAAAGGGGAAAGATTTCTGCAAAAT 1120
Db 120 GTGCCCCCAGGTCCTGAGGTCTGCATCAGGAAAGGGGAAAGATTTCTGCAAAAT 179
QY 1121 GAGAAATAGCTTGGCAGTCCGTTTCCACCCCTGCGAGATGACTCCCGTACTCCCGAGTT 1180
Db 180 GAGAAATAGCTTGGCAGTCCGTTTCCACCCCTGCGAGATGACTCCCGTACTCCCGAGTT 239
QY 1181 AAGAGTGAAGTTCAACAGCCTTCCATCCCAAGCCACTAAGTCCAGATTCCAGAGCCTCC 1240
Db 240 AAGAGTGAAGTTCAACAGCCTTCCATCCCAAGCCACTAAGTCCAGATTCCAGAGCCTCC 299
QY 1241 AGTCTTTCTGAAAGTTCTCTCCCAAGCAATGAAGAAGTTTCAGGCACCTGCAAGAGAG 1300
Db 300 AGTCTTTCTGAAAGTTCTCTCCCAAGCAATGAAGAAGTTTCAGGCACCTGCAAGAGAG 359
QY 1301 ACCTCGGTGGAATGTCAAGAGACAGTCTATCCAATGGAGCGTCTCTTGGCCAAACAGAG 1360
Db 360 ACCTCGGTGGAATGTCAAGAGACAGTCTATCCAATGGAGCGTCTCTTGGCCAAACAGAG 419
QY 1361 GTGTTTTCATCAGCTGCTTCCGTTTGTCTTATTCGAAACAAACTCAGTCTAGGAAACA 1420
Db 420 GTGTTTTCATCAGCTGCTTCCGTTTGTCTTATTCGAAACAAACTCAGTCTAGGAAACA 479

QY	1421	TATGCATCTTTACATGGGAAGAACTCTATTGTAAAGCCTCACITTCATCAACTCAACTCTTTTAAATCT	148
Db	480	TATGCATCTTTACATGGGAAGAACTCTATTGTAAAGCCTCACITTCATCAACTCTTTTAAATCT	539
QY	1481	AAGGCGAACTATGATGAAGGCTTTGGGCACAGACCCACACAGGATCTATGGGCAAGCAAA	1540
Db	540	AAGGCGAACTATGATGAAGGCTTTGGGCACAGACCCACACAGGATCTATGGGCAAGCAAA	599
QY	1541	AATGAAAACGAGAGAGATTTTGGAGAGACCAGCCACAGCTTGCAAAATGCAAGGGAGACCCCT	1600
Db	600	AATGAAAACGAGAGAGATTTTGGAGAGACCAGCCACAGCTTGCAAAATGCAAGGGAGACCCCT	659
QY	1601	CACAGCCCAAGGCTAGAAAGATGCCCTTATTCCTAAAGTGGGTGCTCTGGCTGCAAGTATG	1660
Db	660	CACAGCCCAAGGCTAGAAAGATGCCCTTATTCCTAAAGTGGGTGCTCTGGCTGCAAGTATG	719
QY	1661	GAAGCCAAAGGCTCCTCTCACAGGAGGAAGAACAGCAGCTGAGAAACCAAGAGCTG	1720
Db	720	GAAGCCAAAGGCTCCTCTCACAGGAGGAAGAACAGCAGCTGAGAAACCAAGAGCTG	779
QY	1721	AGGATCGCTGGCCACCCCCACCTGAACTTTGGAAGTTTCAGGAAGTGCCTTGGAGGAAGGG	1780
Db	780	AGGATCGCTGGCCACCCCCACCTGAACTTTGGAAGTTTCAGGAAGTGCCTTGGAGGAAGGG	839
QY	1781	ATCAAAATGTCAAAGCCCAATGSCCTCTGNAAGACGAAATCAGCAAGCCCGGAAGTTCT	1840
Db	840	ATCAAAATGTCAAAGCCCAATGSCCTCTGNAAGACGAAATCAGCAAGCCCGGAAGTTCT	899
QY	1841	GAGGATGTCGATCTAGATCTTGAAGAAGCTTAAGACGATCTTCTTCACTGAAGNAAGCAAGC	1900
Db	900	GAGGATGTCGATCTAGATCTTGAAGAAGCTTAAGACGATCTTCTTCACTGAAGNAAGCAAGC	959
QY	1901	CGCCATTCACTGTAGCAGCTTTCATTTCAAAGCACCTCTGTCAAGAGCCCAAAACTGTG	1960
Db	960	CGCCATTCACTGTAGCAGCTTTCATTTCAAAGCACCTCTGTCAAGAGCCCAAAACTGTG	1019
QY	1961	TCGCCACCTATCAGGAAGGCTGAGCATGTCAGACAGATGAAGAGTCTGTGGGTGGA	2020
Db	1020	TCGCCACCTATCAGGAAGGCTGAGCATGTCAGACAGATGAAGAGTCTGTGGGTGGA	1079
QY	2021	AGAGTTCGAAAGGAACCAAGCTGGAATGCCAAGCTTCTTAAGNAAGATGGGAATGTG	2080
Db	1080	AGAGTTCGAAAGGAACCAAGCTGGAATGCCAAGCTTCTTAAGNAAGATGGGAATGTG	1139
QY	2081	GGAAAAACAACCTGGCAAAACAAAGAACTTAAGGAGAGACAGGGAAGAGAACTAAGAA	2140
Db	1140	GGAAAAACAACCTGGCAAAACAAAGAACTTAAGGAGAGACAGGGAAGAGAACTAAGAA	1199
QY	2141	GGTCATAGTTTGGAGATGGAGAAATGAGAATCTTTGTAAGAAATGGTGACACTCCCATGA	2200
Db	1200	GGTCATAGTTTGGAGATGGAGAAATGAGAATCTTTGTAAGAAATGGTGACACTCCCATGA	1259
QY	2201	GATGATAACAGCTTCTTCAACAAACAAATCTCCACAAAGAACCCCAAGTCTCTGAATTTGGTCG	2260
Db	1260	GATGATAACAGCTTCTTCAACAAACAAATCTCCACAAAGAACCCCAAGTCTCTGAATTTGGTCG	1319
QY	2261	AGTTTTGTAGACAAACCTTTGCTGAAGAAATTCATCTCAGAAATCGAATAATCCAGGAT	2320
Db	1320	AGTTTTGTAGACAAACCTTTGCTGAAGAAATTCATCTCAGAAATCGAATAATCCAGGAT	1379
QY	2321	GTGGAACCTCTGGGAGGGAAGTGGTCAAGAGCTCTCTGTGGAAGAACAGATAAGAGA	2380
Db	1380	GTGGAACCTCTGGGAGGGAAGTGGTCAAGAGCTCTCTGTGGAAGAACAGATAAGAGA	1439
QY	2381	AATCGGTATTATGATGAGGATGAGGATGAAGAGTGACAAATTTGCAATGATCTGGGCTT	2440
Db	1440	AATCGGTATTATGATGAGGATGAGGATGAAGAGTGACAAATTTGCAATGATCTGGGCTT	1499
QY	2441	AAATTCAATGTTAGTGTAGCGAGCCACTGCCCTTTGTCAAAATGTGATGCACATAAGCAG	2500
Db	1500	AAATTCAATGTTAGTGTAGCGAGCCACTGCCCTTTGTCAAAATGTGATGCACATAAGCAG	1559
QY	2501	GTATCCAGCATGAAATGTAATTTACTTTGGAAAGTAACTTTTGGAAAGAAATTTCTTTCTTAA	2560

[illegible]

Db 2640 ATTATATAGAGATTAGCTTTTAATATATTTTTTATAGATGATAAACAATCTGCTTTCTTAGTC 2699

Qy 3641 TTACTAGTCTGAACAACATTTTATTCATAAAGATTTTAATTAATTTG 3690

Db 2700 TTACTAGTCTGAACAACATTTTATTCATAAAGATTTTAAATTTG 2749

RESULT 6

US-09-925-297-152

Sequence 152, Application US/09925297

Patent No. US20020081659A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA105

CURRENT APPLICATION NUMBER: US/09/925,297

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05989

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 928

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 152

LENGTH: 732

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: (729)

OTHER INFORMATION: n equals a.t.g, or c

US-09-925-297-152

Query Match 19.5%; Score 722; DB 9; Length 732;

Best Local Similarity 99.3%; Pred. No. 7.9e-166;

Matches 719; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 GGAAGGGGAAAAGATTCTGCAAAATGAGATAGCGTGGCAGTCCGTTCCACCCCTGCCGA 1155

Db 1 GGAAGGGGAAAAGATTCTGCAAAATGAGATAGCGTGGCAGTCCGTTCCACCCCTGCCGA 60

Qy 1156 AGATGACTCCCGTACTCCAGGTTAAGAGTGAAGTTCACAGCGCTGCATCCCAAGCC 1215

Db 61 AGATGACTCCCGTACTCCAGGTTAAGAGTGAAGTTCACAGCGCTGCATCCCAAGCC 120

Qy 1216 ACTAAGTCAGATTCCAGAGCCTCAGTCTTTCTGAAAGTTCCTCCCAAGCAATGAA 1275

Db 121 ACTAAGTCAGATTCCAGAGCCTCAGTCTTTCTGAAAGTTCCTCCCAAGCAATGAA 180

Qy 1276 GAAGTTTCAGGCACCTGCAAGAGAGACCTGCGTGAATGTCAGAAGACAGTCTATCCAAT 1335

Db 181 GAAGTTTCAGGCACCTGCAAGAGAGACCTGCGTGAATGTCAGAAGACAGTCTATCCAAT 240

Qy 1336 GGAGCGTCTCTTTGGCCAACCCAGCAGGTGTTTCACATCAGCTGCTTCGGTTCCTATTG 1395

Db 241 GGAGCGTCTCTTTGGCCAACCCAGCAGGTGTTTCACATCAGCTGCTTCGGTTCCTATTG 300

Qy 1396 CAACAACAAACTCAGTCTAGGAACATATGCAATCTTTACATGGAAGATCTATTGTAAGCC 1455

Db 301 CAACAACAAACTCAGTCTAGGAACATATGCAATCTTTACATGGAAGATCTATTGTAAGCC 360

Qy 1456 TCACCTTCATCAACTCTTTAATCTTAAGGGCAACTATGATGAAGCTTTGGGCACAGACC 1515

Db 361 TCACCTTCATCAACTCTTTAATCTTAAGGGCAACTATGATGAAGCTTTGGGCACAGACC 420

Qy 1516 ACACAAGGATCTATGGGCAAGCAAAATGAAAACGAGAGATTTTGGAGACCCAGCCCA 1575

Db 421 ACACAAGGATCTATGGGCAAGCAAAATGAAAACGAGAGATTTTGGAGACCCAGCCCA 480

Qy 1576 GCTTGCAATGCAAGGGAGACCCCTTCACAGCCCGGGGTAGAAGATGCCCTATTGCTAA 1635

Db 481 GCTTGCAATGCAAGGGAGACCCCTTCACAGCCCGGGGTAGAAGATGCCCTATTGCTAA 540

Qy 1636 GGTGGGTCTCTGGCTGCAAGTATGGAAGCCAAAGCCTCTCTCAGCAGGAGAAGGAAGA 1695

Db 541 GGTGGGTCTCTKCTGCAAGTATGGAAGCCAAAGCCTCTCTCAGCAGGAGAAGGAAGA 600

Qy 1696 CAAGCCAGCTGAACCAACAAGAGCTGAGGATCGCTGGCCACCCCCCTGAACTTGGAG 1755

Db 601 CAAGCCAGCTGAACCAACAAGAGCTGAGGATCGCTGGCCACCCCCCTGAACTTGGAG 660

Qy 1756 TTCAGGAAGTCCCTTGGAGGAAGGATCAAAATGTCAAAGCCCAAAATGCCCTCTCTGAAGA 1815

Db 661 TTCAGGAAGTCCCTTGGAGGAAGGATCAAAATGTCAAAGCCCAAAATGCGCTCTCTGAAGA 720

Qy 1816 CGAA 1819

Db 721 CGAA 724

RESULT 7

US-10-198-846-10895

Sequence 10895, Application US/10198846

Publication No. US2003009974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Xu, Yongyao

APPLICANT: Wang, Youzhen

APPLICANT: Steinmann, Kathleen

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: THERAPY OF BREAST CANCER

FILE REFERENCE: MRI-049

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10895

LENGTH: 698

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1, 2, 691, 692, 693, 694, 695, 696, 697, 698

OTHER INFORMATION: n = A,T,C or G

US-10-198-846-10895

Query Match 15.9%; Score 590.6; DB 15; Length 698;

Best Local Similarity 92.8%; Pred. No. 1e-133;

Matches 649; Conservative 0; Mismatches 4; Indels 46; Gaps 1;

Qy 1 GGCGCAGGAGCAGTAGGTTGTTAGCAGCTTGGTCGCGACAGGTGCGCTAGGTAGAGCGCC 60

Db 38 GGCGCAGGAGCAGTAGGTTGTTAGCAGCTTGGTCGCGACAGGTGCGCTAGGTAGAGCGCC 97

Qy 61 GGACCTGTGACAGGCTGGTAGCAGAGGAAAGCGGCTTTTAGCCAGGTATTTC 120

Db 98 GGACCTGTGACAGGCTGGTAGCAGAGGAAAGCGGCTTTTAGCCAGGTATTTC 157

Qy 121 AGTGTCTGTAGACAAGATGGAATCATCTCCATTTAATAGACGCAATGGACCTCACTATC 180

Db 158 AGTGTCTGTAGACAAGATGGAATCATCTCCATTTAATAGACGCAATGACCTCACTATC 217

Qy 181 ATTGAGGTTAAGCCAAAGAACTTTCTCTTGTCAACAAGAACAGTCACTGCTATTGT 240

Db 218 ATTGAGGTTAAGCCAAAGAACTTTCTCTTGTCAACAAGAACAGTCACTGCTATTGT 277

Qy 241 GGAATATTCTCCAGTACCAGAAACGACTGGAAGAAACAAACATGGAGAAAGAGAAG 300

Db 278 GGAATATTCTCCAA----- 292

Qy 301 TAACACCGAAAAATCTCTCCAGCACTTTTAAAGGGGACCCCTGACTGTGTTTAAAGAGAA 360

Db 293 -AACACCGAAAAATCTCTCCAGCACTTTTAAAGGGGACCCCTGACTGTGTTTAAAGAGAA 351

Qy	361	GTGGGAAACCCAGGCGCTGGGAGCAGAGTCTCACACAGACTCTCTACGGAAACAGCAGCAC	420
Db	352	GTGGGAAACCCAGGCGCTGGGAGCAGAGTCTCACACAGACTCTCTACGGAAACAGCAGCAC	411
Qy	421	TGAGATTAGGCACAGACAGACCATCTCTCTGCTGAAGTGACAAGCCACGCTCTCTGG	480
Db	412	TGAGATTAGGCACAGACAGACCATCTCTCTGCTGAAGTGACAAGCCACGCTCTCTGG	471
Qy	481	AGCCAAAGGTGACCAAGAGAGAACAAATCCACCCAGATCTAGACTCAGGTCACTCTCTGA	540
Db	472	AGCCAAAGGTGACCAAGAGAGAACAAATCCACCCAGATCTAGACTCAGGTCACTCTCTGA	531
Qy	541	AGCCCTCGTTCAAGGTCGATATCCCCACATCAAGGACGGTGAAGATCTTAAAGACCACTC	600
Db	532	AGCCCTCGTTCAAGGTCGATATCCCCACATCAAGGACGGTGAAGATCTTAAAGACCACTC	591
Qy	601	AACAGAAATGAAAAAATGGAAAAATTGCTTAGGAGAAATCCAGGCATGAAGTAGAAAAATC	660
Db	592	AACAGAAATGAAAAAATGGAAAAATTGCTTAGGAGAAATCCAGGCATGAAGTAGAAAAATC	651
Qy	661	AGAAATTCAGTGAACACAGATGCTTCGGGCAAAATAGA	699
Db	652	AGAAATTCAGTGAACACAGATGCTTCGGGCAAAATAGA	690

RESULTS

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US/060-036-4338
; Sequence 4338, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Lodes, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, yugui
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; FOR THE TREATMENT OF CANCER
; TITLE OF INVENTION: AND DIAGNOSIS OF PAN
; FILE REFERENCE: 210121,566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4338
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 416, 418, 556
; OTHER INFORMATION: n = A,T,C or G
US-10-060-036-4338

```

	Query Match	14.9%	Score 551;	DB 15;	Length 565;
	Best Local Similarity	99.5%;	Pred. No. 4.4e-124;		
	Matches 562;	Conservative 0;	Mismatches 2;	Indels 1;	Gaps 1;
1925	QY	TTTCAAAGCACCTCTGTC	CAAGAGCCCAAAA	CTGTCTCCCA	CTATCAGGAAAGGCTGG
	Db	TTTCAAAGCACCTCTGTC	CAAGAGCCCAAAA	CTGTCTCCCA	CTATCAGGAAAGGCTGG
1	QY	AGCATGTCAGAGCAGAGTGAAG	AGTCTGTGGT	TGGAAGAGTTCAGAAAGGAAACAAAGT	2044
	Db	AGCATGTCAGAGCAGAGTGAAG	AGTCTGTGGT	TGGAAGAGTTCAGAAAGGAAACAAAGT	2044
61	QY	AAAAATGCCAAGGCTTCTAAG	AGAAGAAATGGGAAT	TGGGAAAAACAACTG	GCACAAACAA
	Db	AAAAATGCCAAGGCTTCTAAG	AGAAGAAATGGGAAT	TGGGAAAAACAACTG	GCACAAACAA
2045	QY	AAAAATGCCAAGGCTTCTAAG	AGAAGAAATGGGAAT	TGGGAAAAACAACTG	GCACAAACAA
	Db	AAAAATGCCAAGGCTTCTAAG	AGAAGAAATGGGAAT	TGGGAAAAACAACTG	GCACAAACAA
121	QY	GAATCTAAAGAGAGACACGG	AGAGCAAGT	TAGGAGAGTTCATAGTTGGAGATGGAGAAT	2164
	Db	GAATCTAAAGAGAGACACGG	AGAGCAAGT	TAGGAGAGTTCATAGTTGGAGATGGAGAAT	2164
2105	QY	GAATCTAAAGAGAGACACGG	AGAGCAAGT	TAGGAGAGTTCATAGTTGGAGATGGAGAAT	240
	Db	GAATCTAAAGAGAGACACGG	AGAGCAAGT	TAGGAGAGTTCATAGTTGGAGATGGAGAAT	240

QY	2165	GAGAAATCTTTGAGAAAATGGTGCAGACTCCGATGAAGATGATAACAGCTTCTCCTCAACAA	2254
Db	241	GAGAAATCTTTGAGAAAATGGTGCAGACTCCGATGAAGATGATAACAGCTTCTCCTCAACAA	300
QY	2225	CAATCTCCACAAGAACCCAGATCTCTCGAATTGGTCGAGTTTGTAGACAACACCTTTGCT	2284
Db	301	CAATCTCCACAAGAACCCAGATCTCTCGAATTGGTCGAGTTTGTAGACAACACCTTTGCT	360
QY	2285	GAGAAATTCACACTCTCAGATTCAGAAATCCAGGATGTGGAATCTCGGAGGGAG - AAGT	2343
Db	361	GAGAAATTCACACTCTCAGATTCAGAAATCCAGGATGTGGAATCTCGGAGGGAGNAGT	420
QY	2344	GGTCAAAAGAGCTCTCTGTGGAAGAACAGATAAAGAGAAATCGGTATTATCATGAGGATGA	2403
Db	421	GGTCAAAAGAGCTCTCTGTGGAAGAACAGATAAAGAGAAATCGGTATTATCATGAGGATGA	480
QY	2404	GGATGAAGAGTGCACAAATTGCAATGATGCTGGGCCCTTAAATTCATGTTAGTTAGCGAG	2463
Db	481	GGATGAAGAGTGCACAAATTCGAATGATGCTGGGCCCTTAAATTCATGTTAGTTAGCGAG	540
QY	2464	CCACTGCCCTTTGTCAAAATGTGAT	2488
Db	541	CCACTGCCCTTTGTCAAAATGTGAT	565

RESULT 9

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US-10-066-543-3373
; Sequence 3373, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuguu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Sectist, Heather
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF COLON CANCER
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066.543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3373
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 534
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-3373

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Query Match	14.8%	Score 548.8;	DB 15;	Length 583;
Best Local Similarity	97.8%	Pred. No. 1.5e-123;		
Matches 580; Conservative	0;	Mismatches 3;	Indels 10;	Gaps 2;

QY	2543	AAAAGAATTCCCTTCTTAAAAATCAAAACAAAAACAAAAACACAAAAACACATTTCTTAAA	2602
Db	1	AAAAGAATTCCCTTCTTAAAAATCAAAACAAAAACA	51
QY	2603	TACTAGAGATAACTTTTACTTAAATTTCTTCATTTTACGAGTGATGATGCATAAGTGCTG	2662
Db	52	TACTAGAGATAACTTTTACTTTAAATTTCTTCATTTTACGAGTGATGATGCATAAGTGCTG	111
QY	2663	TAGGCGTTGTAAGTGGGAAATATTTCCACCTGATATAATAGCCAGATTTCTACTGTATTCCC	2722

Db	52	TACTAGAGTAACCTTTTACTTAATCTCTCAATTTTACGAGTGATGATGATCATGAAGTCGTG	111
QY	2663	TAAAGCTTTGTAACCTGGGGAATAATTCACACCTGATAATAGCCAGATCTTACTGTATTCCTC	2722
Db	112	TAAAGCTTTGTAACCTGGGGAATAATTCACACCTGATAATAGCCAGATCTTACTGTATTCCTC	171
QY	2723	AAAAGGCAATATTAAAGGTAGATAGATGATTAGTAGTATATTGTTACACACTATTTTGGAA	2782
Db	172	AAAAGGCAATATTAAAGGTAGACAGATGATTAGTAGTATATTGTTACACACTATTTTGGAA	231
QY	2783	TTAGAGAACATACAGAAGGAATTTAGGGGCTTTAAACATTACGACTGAATGCCACTTTAGTA	2842
Db	232	TTAGAGAACATACAGAAGGAATTTAGGGGCTTTAAACATTACGACTGAATGCCACTTTAGTA	291
QY	2843	TAAAGGCAAGATTTGTATATTTTAAATGAATACCAATTTAAATTTTGTAGTATTACCT	2902
Db	292	TAAAGGCAAGATTTGTATATTTTAAATGAATACCAATTTAAATTTTGTAGTATTACCT	351
QY	2903	GTTAAGAGATATTAGTCTTTTAAATTTTGTAGTAAATTTTCTTGCTGTGATATATG	2962
Db	352	GTTAAGAGATATTAGTCTTTTAAATTTTGTAGTAAATTTTCTTGCTGTGATATATG	411
QY	2963	AGGAATTTACTCTTTATGTCCTGCTCTCTAACTACATCTTGAACCTCGACGCTCTGAGG	3022
Db	412	AGGAATTTACTCTTTATGTCCTGCTCTCTAACTACATCTTGAACCTCGACGCTCTGAGG	471
QY	3023	TATAATACACAGAGCACATTTTGGGGCAATTTGAAACCAACCTACACTCTTCGGTGCT	3082
Db	472	TATAATACACAGAGCACATTTTGGGGCAATTTGAGGCAATG-AAAACCACTTACACTCTTCGGTGCT	530
QY	3083	TAGAGAGATCTGCTGTC	3099
Db	531	TANAGAGATCTGCTGTC	547

RESULT 11

US-09-918-995-7225

; Sequence 7225, Application US/09918995

; Publication No. US20030073623A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US/09/235,076

; PRIOR FILING DATE: 1999-01-20

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7225

; LENGTH: 404

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-918-995-7225

Query Match 10.3%; Score 383.2; DB 11; Length 404;

Best Local Similarity 96.8%; Pred No. 3.8e-83;

Matches 391; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY	3168	ATATCTGCTCTTCATAATTACTGAAAGCTGCAATATTTTAGTAATACCTTCGGGATCA	3227
Db	1	ATATCTGCGCTTCTCATAATTACTGAAAGCTGCTTTATTTTAGTAATACCTTCGGGACCA	60
QY	3228	CTGTCCCCCATCTTCGGTGTGTAGACCAAGTGAAGAGTTTAAAGGAGGAAGAAAGAA	3287
Db	61	CTGTGCCCCATCTTCGGTGTGTAGACCAAGTGAAGAGTTTAAAGGAGGAAGAAAGAA	120
QY	3288	CTGTCTTTACACCACTTGAGCTCAGACCTCTAAACCCCTGATTTTCCCTTATGATGTC	3347
Db	121	CTGTCTTTACACCACTTGAGCTCAGACCTCTAAACCCCTGATTTTCCCTTATGATGTC	180

QY 3348 TTTTGAGACACTAATTTTAAATACCTTACTAGCTCTGAAATATATTGATTTTATACAG 3407
Db 181 TTTTGAGACACTAATTTTAAATACCTTACTAGCTCTGAAATATATTGATTTTATACAG 240
QY 3408 TATTTCTCAGGTGAAATTAACCAACTATAGGCTTTTCTTGGGATGATTTTCTAGTCT 3467
Db 241 GCTTCTCAGGTGAAATTAACCAACTATAGGCTTTTCTTGGGATGACATTTCTAGTCT 300
QY 3468 TAAAGTTTGGGACATTTATAACCTTGAGTACATTTGTTGTACACAGTTGATATCCAAAT 3527
Db 301 TAAAGTTTGGGACATTTATAACCTTGAGTACATTTGTTGTACACAGTTGATATCCACAT 360
QY 3528 TGTATGATGGAGGAGGAGGTGCTTTAAAGTGTAGGCTTTTCT 3571
Db 361 TCCATGGATGGAGGAGGAGGTGCTTTAAAGTGTAGGCTTCT 404

RESULT 12

US-09-918-995-7296
; Sequence 7296, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7296
; LENGTH: 410
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-7296

Query Match 10.1%; Score 374.4; DB 11; Length 410;
Best Local Similarity 94.9%; Pred. No. 5.4e-81;
Matches 387; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 3167 GATATCTGTGCTTCTCATAATTACTGAAAGCTGCAATATTTTAGTAAATACCTTCGGGATC 3226
Db 2 GATATCTGTGCTTCTCATAATTACTGAAAGCTGCAATATTTTAGTAAATACCTTCGGGATC 61
QY 3227 ACTGTCCCCCATCTTCGTTTAGACAAAGTGAAGAGTTTAAAGGAGGAAGAAAGA 3286
Db 62 ACTGTCCCGCATGTCGCTGTTGAGCAAAGGAGAGAGCTTAAAGGAGGAAGAGATGA 121
QY 3287 ACTGTCTTACACCACTTGAGCTCAGACCCTTAAACCTGTAATTTCCCTTATGATGTCCTC 3346
Db 122 ACTGTCTTACACCACTTGAGCTCAGACCCTTAAACCTGTAATTTCCCTTATGATGTCCTC 181
QY 3347 TTTTTCGACACACTAATTTTAAATACCTTACTAGCTCTGAAATATATTGATTTTATCACA 3406
Db 182 TTTTTCGACACACTAATTTTAAATACCTTACTAGCTCTGAAATATATTGATTTTATCACA 241
QY 3407 GTATTTCTCAGGGTGAATTAACCAACTATAGGCTTTTCTTGGGATGATTTTCTAGTC 3466
Db 242 GTATTTCTCAGGGTGAATTAACCAACTATAGGCTTTTCTTGGGATGATTTTCTAGTC 301
QY 3467 TTAAGGTTTGGGACATTTATAACCTTGAGTACATTTGTTGTACACAGTTGATATCCAAA 3526
Db 302 TTAAGGATTTGGGACATTTATAACCTTGAAATACATATGCTGGACACAGTTGATATCCAAA 361
QY 3527 TTGTATGGATGGAGGAGGAGGTGCTTAAAGTGTAGGCTTTTCTTTG 3574
Db 362 TTGTATGGATGGAGGAGGAGGTGCTTAAAGTGTAGGCTTATTTCTTTG 409

RESULT 13

US-09-871-161-139/c

; Sequence 139, Application US/09871161
; Publication No. US20030097666A1
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCNA-260XX
; CURRENT APPLICATION NUMBER: US/09/871,161
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 09/328,111
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/117,393
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/098,639
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 139
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(586)
; OTHER INFORMATION: n = A,T,C or G
US-09-871-161-139

Query Match 9.8%; Score 362; DB 11; Length 586;
Best Local Similarity 100.0%; Pred. No. 7.4e-78;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3137 GTACTCCAAATGATTGCTTTCTTTCTGGTGATATCTGTGCTTCTCATAATTACTGAAAG 3196
Db 363 GTACTCCAAATGATTGCTTTCTTTCTGGTGATATCTGTGCTTCTCATAATTACTGAAAG 304
QY 3197 CTGCAATATTTTAGTAATACCTTCGGGATCACTGCCCATCTTCCGTTGTAGAGCAA 3256
Db 303 CTGCAATATTTTAGTAATACCTTCGGGATCACTGCCCATCTTCCGTTGTAGAGCAA 244
QY 3257 GTGAAGAGTTTAAAGGAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 3316
Db 243 GTGAAGAGTTTAAAGGAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 184
QY 3317 TAAACCCCTGTATTTCCCTTATGATCTCCCTTTTATGACACTAATTTTAAATACCTTAC 3376
Db 183 TAAACCCCTGTATTTCCCTTATGATCTCCCTTTTATGACACTAATTTTAAATACCTTAC 124
QY 3377 TAGCTCTGAAATATATTGATTTTATCAGATTTCTCAGGTGAAATTAACCAACTAT 3436
Db 123 TAGCTCTGAAATATATTGATTTTATCAGATTTCTCAGGTGAAATTAACCAACTAT 64
QY 3437 AGGCTTTTCTTGGGATGATTTTCTAGTCTTAAAGTTTGGGACATTTAAACTTTGAGT 3496
Db 63 AGGCTTTTCTTGGGATGATTTTCTAGTCTTAAAGTTTGGGACATTTAAACTTTGAGT 4
QY 3497 AC 3498
Db 3 AC 2

RESULT 14

US-10-066-543-1533/c
; Sequence 1533, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.

APPLICANT: Smith, Carole L.
APPLICANT: Durham, Margarita
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.563
CURRENT APPLICATION NUMBER: US/10/066,543
CURRENT FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1533
LENGTH: 358
TYPE: DNA
ORGANISM: Homo sapiens
US-10-066-543-1533

Query Match
Best Local Similarity 100.0%; Score 358; DB 15; Length 358;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3139 ACTCCAAATGATGCTTCTTTCTTGGTGATATCTGTGTTCTCATAATTACTGAAAGCT 3198
DB 358 ACTCCAAATGATGCTTCTTTCTTGGTGATATCTGTGTTCTCATAATTACTGAAAGCT 299
QY 3199 GCAATATTTTAGTAATACCTTCGGGATCACTGTCCTCCCATCTTCGGTGTAGAGCAAAAGT 3258
DB 298 GCAATATTTTAGTAATACCTTCGGGATCACTGTCCTCCCATCTTCGGTGTAGAGCAAAAGT 239
QY 3259 GAAGAGTTTTAAAGGAGGAAGAAGAACTGCTTTACACCACTTTGAGCTCAGACCTCTA 3318
DB 238 GAAGAGTTTTAAAGGAGGAAGAAGAACTGCTTTACACCACTTTGAGCTCAGACCTCTA 179
QY 3319 AACCTGTATTTCCCTTATGATGTGCCCTTTTGAGACACTAAATTTTAAATACTTACTA 3378
DB 178 AACCTGTATTTCCCTTATGATGTGCCCTTTTGAGACACTAAATTTTAAATACTTACTA 119
QY 3379 GCTCTGAATATATTGATTTTATCAGACTATTTCTCAGGGTGAATTTAAACCACTATAG 3438
DB 118 GCTCTGAATATATTGATTTTATCAGACTATTTCTCAGGGTGAATTTAAACCACTATAG 59
QY 3439 GCCTTTTCTTGGGATGATTTTCTAGTCTTAAGTTTGGGACATTTAAACTTGAGT 3496
DB 58 GCCTTTTCTTGGGATGATTTTCTAGTCTTAAGTTTGGGACATTTAAACTTGAGT 1

RESULT 15
US-09-998-598-1767/c
Sequence 1767, Application US/09998598
Patent No. US2002015092A1
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.561
CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 1767
LENGTH: 283
TYPE: DNA
ORGANISM: Homo sapiens
US-09-998-598-1767

Query Match
Best Local Similarity 99.3%; Score 279.8; DB 10; Length 283;
Matches 281; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2585 CAAAAACACATTCTAAATAGTAGTACTTTTCTTAAATTTCTTCAATTTAGCAGTGA 2644
|||||

Search completed: January 6, 2004, 16:13:03
Job time : 1111 secs

Db 283 CAAAAACACATTCTAAATAGTAGTAACTTTTACTTTAAATTTCTTCAATTTAGCAGTGA 224
QY 2645 TGATATGCATAAGTGCTGTAAAGGCTTGTAACTGGGAAATATTCCACCTGATAATAGCCC 2704
Db 223 TGATATGCATAAGTGCTGTAAAGGCTTGTAACTGGGAAATATTCCACTGATAATAGCCC 164
QY 2705 AGATTCTACTGTATTCCCAAAAGGCAATATTAAAGGTAGATAGATTAGTAGTATATTG 2764
Db 163 AGATTCTACTGTATCCCAAAAGGCAATATTAAAGGTAGATAGATTAGTAGTATATTG 104
QY 2765 TTACACACTATTTTGGGAATTAGAGAAACATACAGAAAGAAATTTAGGGGCTTAAACATTACG 2824
Db 103 TTACACACTATTTTGGGAATTAGAGAAACATACAGAAAGAAATTTAGGGGCTTAAACATTACG 44
QY 2825 ACTGAATGCACCTTTTAGTATATAAGGGCACAGTTTGTATATTTTT 2867
Db 43 ACTGAATGCACCTTTTAGTATATAAGGGCACAGTTTGTATATTTTT 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run On: January 6, 2004, 10:12:26 ; Search time 903 Seconds
(without alignments)
11075.767 Million cell updates/sec

Title: US-09-890-549-16
Perfect score: 3705
Sequence: 1 ggcgcaggagcagtaggtgatttgaaaaaaaaaaaaa 3705

Scoring table: OLIGO NUC
Gapop 60.0, Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_19Jun03.:

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- 2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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- 22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
- 23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3705	100.0	3705	21	Sequence encoding
2	3611	97.5	3664	23	Human transcriptio
3	3412	92.1	3711	21	Human OREF ORF3698
4	2596	70.1	2783	20	Human breast tumo
5	2589	69.9	2749	24	Human cDNA encodin
6	2565	69.2	2905	22	Human polynucleoti
7	2130	57.5	3650	22	Human EPLIN (epith
8	2092	56.5	2267	21	Human secreted pro

9	2041	55.1	3543	22	AAF555696	Human EPLIN (epith
10	1519	41.0	2207	22	AAH18125	Human cDNA sequenc
11	1310	35.4	1713	22	AAI59955	Human polynucleoti
12	1296	35.0	1754	24	ABI98973	Human cancer supp
13	1269	34.3	2158	21	AAI59973	Human secreted pro
14	1186	32.0	1567	24	AAI58588	Human secreted pro
15	604	16.3	641	20	AAI525892	Human secreted pro
16	590	15.9	3465	23	AAI525892	Human prostate tum
17	556	15.0	732	21	AAI525892	Human secreted pro
18	466	12.6	1014	23	AAI525892	Human secreted pro
19	415	11.2	565	24	AAI525892	Human secreted pro
20	385	10.4	698	22	AAI525892	Human secreted pro
21	362	9.8	586	21	AAI525892	Human secreted pro
22	343	9.3	343	24	AAI525892	Human secreted pro
23	343	9.3	343	24	AAI525892	Human secreted pro
24	340	9.2	463	24	AAI525892	Human secreted pro
25	335	8.8	389	21	AAI525892	Human secreted pro
26	314	8.5	376	21	AAI525892	Human secreted pro
27	276	7.4	279	25	AAI525892	Human secreted pro
28	248	6.7	413	25	AAI525892	Human secreted pro
29	236	6.4	532	22	AAI525892	Human secreted pro
30	230	6.2	419	22	AAI525892	Human secreted pro
31	216	5.8	408	23	AAI525892	Human secreted pro
32	212	5.7	247	22	AAI525892	Human secreted pro
33	209	5.6	231	22	AAI525892	Human secreted pro
34	209	5.6	255	22	AAI525892	Human secreted pro
35	208	5.6	265	22	AAI525892	Human secreted pro
36	186	5.0	283	24	AAI525892	Human secreted pro
37	175	4.7	178	24	AAI525892	Human secreted pro
38	164	4.4	2226	23	AAI525892	Human secreted pro
39	158	4.3	382	24	AAI525892	Human secreted pro
40	153	4.2	232	22	AAI525892	Human secreted pro
41	143	3.9	296	21	AAI525892	Human secreted pro
42	140	3.8	269	22	AAI525892	Human secreted pro
43	136	3.7	996	23	AAI525892	Human secreted pro
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45	119	3.2	238	25	AAI525892	Human secreted pro

ALIGNMENTS

RESULT 1	AAI53826	standard; DNA; 3705 BP.
ID	AAI53826	standard; DNA; 3705 BP.
XX	AAI53826;	
AC	AAI53826;	
XX	03-JAN-2001	(first entry)
DT	03-JAN-2001	(first entry)
DE	Sequence encoding lipid associated protein (LIPAP) 2766980CB1.	
XX	Lipid associated protein; LIPAP; treatment; prophylaxis; agonist;	
XX	antagonist; antibody; cardiovascular disease; neurological disease;	
XX	gastrointestinal disease; lipid metabolism; detection;	
XX	amplification; monitoring; hybridisation; antisense; triplex;	
XX	ribozyme; screening; immunoassay; ds.	
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
FT	CDS	137..2416
FT		/*tag= a
FT		/product= Lipid associated protein
XX	WO200049043-A2.	
PN	24-AUG-2000.	
PD	18-FEB-2000; 2000WO-US04160.	
PP	19-FEB-1999; 99US-0120703.	
XX	08-JUL-1999; 99US-0142762.	
PR		

XX PA (INCY-) INCYTE PHARM INC.
XX PI Tang YT, Hillman JL, Yue H, Azimzai Y, Baughn MR, Tran B;
XX DR WPI; 2000-549264/50.
XX DR P-PSDB; AAY97286.
XX PT New human lipid-associated proteins, nucleic acids, and antibodies,
XX PT useful for diagnosis, treatment and prevention of e.g. cardiovascular
XX PT disease
XX PS Claim 4; Page 87-88; 93pp; English.
XX CC Lipid-associated proteins (LIPAP) can be used for treating or
XX CC preventing disorders associated with decreased expression of LIPAP,
XX CC for screening for agonists or antagonists of LIPAP, and to raise
XX CC specific antibodies. Antagonists and agonists of LIPAP are useful
XX CC for treating diseases associated with reduced or increased levels of
XX CC LIPAP, e.g. cardiovascular, neurological and gastrointestinal
XX CC diseases and disorders of lipid metabolism. Fragments of the nucleic
XX CC acid encoding LIPAP are useful for detection of full length coding
XX CC sequences, in hybridization and/or amplification assays or for
XX CC diagnosis or monitoring. Nucleotides encoding LIPAP are used
XX CC to screen for compounds that specifically modify LIPAP expression,
XX CC for recombinant production of LIPAP, in gene therapy, as a source of
XX CC therapeutic antisense, triplex-forming, or ribozyme agents and for
XX CC genomic mapping. Antibodies to the proteins are used for diagnosis
XX CC and monitoring of LIPAP-associated disease by immunoassay, as
XX CC antagonists, in competitive drug screens and for affinity
XX CC purification of natural LIPAP.
XX SQ Sequence 3705 BP; 1217 A; 743 C; 826 G; 919 T; 0 other;

Query Match 100.0%; Score 3705; DB 21; Length 3705;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGCAGGAGCAGTAGGTTAGCAGCTTGGTCGCGACAGTGCGCTAGGTAGAGCC 60
Db |||||
QY 1 GCGCGCAGGAGCAGTAGGTTAGCAGCTTGGTCGCGACAGTGCGCTAGGTAGAGCC 60
Db |||||
QY 61 GGGACCTGTGACAGGCGCTGGTAGCAGCGCAGAGGAAAGCGGCTTTAGCCAGGTATTC 120
Db |||||
QY 61 GGGACCTGTGACAGGCGCTGGTAGCAGCGCAGAGGAAAGCGGCTTTAGCCAGGTATTC 120
Db |||||
QY 121 AGTGCTGTGACAGAGATGGAAATCATCTCCATTTAATAGACGGCAATGGACCTCACTATC 180
Db |||||
QY 121 AGTGCTGTGACAGAGATGGAAATCATCTCCATTTAATAGACGGCAATGGACCTCACTATC 180
Db |||||
QY 181 ATTGAGGCTAACAGCAAGAACTTTCTTGTGTAACAGAAACAGTCATCGGCTATTGT 240
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QY 181 ATTGAGGCTAACAGCAAGAACTTTCTTGTGTAACAGAAACAGTCATCGGCTATTGT 240
Db |||||
QY 241 GGAATATTCTCCAGTACCAGAAAGCAGCTGAAGAAACATGGAAGAGAGAAAG 300
Db |||||
QY 241 GGAATATTCTCCAGTACCAGAAAGCAGCTGAAGAAACATGGAAGAGAGAAAG 300
Db |||||
QY 301 TAACACCGAAATCTCTCCAGCACTTTAGAAAGGGACCTGACTGTGTTAAGAGAGAA 360
Db |||||
QY 301 TAACACCGAAATCTCTCCAGCACTTTAGAAAGGGACCTGACTGTGTTAAGAGAGAA 360
Db |||||
QY 361 GTGGAGAACCCAGGCTGGGAGCAGAGTCTCACAGACTCTCTACGGAAACAGCAC 420
Db |||||
QY 361 GTGGAGAACCCAGGCTGGGAGCAGAGTCTCACAGACTCTCTACGGAAACAGCAC 420
Db |||||
QY 421 TGAGATTAGGCACAGACAGCCATCTCTGCTGAAGTGACAAAGCCACCTCTTCTGG 480
Db |||||
QY 421 TGAGATTAGGCACAGACAGCCATCTCTGCTGAAGTGACAAAGCCACCTCTTCTGG 480
Db |||||
QY 481 AGCCAAAGCTGACCAAGAAAGAAATTCACCCCGAGATCTAGACTCAGGTCACTCTGTA 540
Db |||||
QY 481 AGCCAAAGCTGACCAAGAAAGAAATTCACCCCGAGATCTAGACTCAGGTCACTCTGTA 540
Db |||||

QY 541 AGCCCTCGTTGAGGTCGATATCCCCACATCAAGACGGTGAGGATCTTAAAGACCACTC 600
Db |||||
QY 541 AGCCCTCGTTGAGGTCGATATCCCCACATCAAGACGGTGAGGATCTTAAAGACCACTC 600
Db |||||
QY 601 AACAGAAAGTAAAGAAATGGAAATTTGCTAGGAGAAATCCAGGATGAAGTAGAAAAATC 660
Db |||||
QY 601 AACAGAAAGTAAAGAAATGGAAATTTGCTAGGAGAAATCCAGGATGAAGTAGAAAAATC 660
Db |||||
QY 661 AGAAATCAGTGAAGAACACAGATGCTTCGGGCAAAATAGAGAAATATATATGTTCCGCTGAA 720
Db |||||
QY 661 AGAAATCAGTGAAGAACACAGATGCTTCGGGCAAAATAGAGAAATATATATGTTCCGCTGAA 720
Db |||||
QY 721 CAGGCTTAAGATGATGTTTGAGAAAGGTGAACCAACTCAAACTAAGATTTCTCCGGGCCA 780
Db |||||
QY 721 CAGGCTTAAGATGATGTTTGAGAAAGGTGAACCAACTCAAACTAAGATTTCTCCGGGCCA 780
Db |||||
QY 781 AAGCGAAGTCAAGTGAAGAAAGATCTCTGAAAAACAGCTATTCTCTAGATGACCTGGA 840
Db |||||
QY 781 AAGCGAAGTCAAGTGAAGAAAGATCTCTGAAAAACAGCTATTCTCTAGATGACCTGGA 840
Db |||||
QY 841 AATAGGCCAGGTCAGTTGTCATCTTACATTTGACTCGGAGAAAAATGAGAGTAGACG 900
Db |||||
QY 841 AATAGGCCAGGTCAGTTGTCATCTTCTACATTTGACTCGGAGAAAAATGAGAGTAGACG 900
Db |||||
QY 901 AAATCTGGAATCTCCACGCTCTCAGAAACCTCTATTAAGGATCGAATGCGCAAGTACCA 960
Db |||||
QY 901 AAATCTGGAATCTCCACGCTCTCAGAAACCTCTATTAAGGATCGAATGCGCAAGTACCA 960
Db |||||
QY 961 GGCAGCTGTGTCACAAACAAAGCAGCTCAACCAACTATACAAATGAGCTGAAAGCCAGTGG 1020
Db |||||
QY 961 GGCAGCTGTGTCACAAACAAAGCAGCTCAACCAACTATACAAATGAGCTGAAAGCCAGTGG 1020
Db |||||
QY 1021 TGGCGAAATCAAAATTCATTAATTAAGGAGCAAAAGGAAATGTGCCCCAGGTCCTGAGGT 1080
Db |||||
QY 1021 TGGCGAAATCAAAATTCATTAATTAAGGAGCAAAAGGAAATGTGCCCCAGGTCCTGAGGT 1080
Db |||||
QY 1081 CTGCATCACCCATCAGAGAGGGGAAAGATTTCTGCAAAATGAGAAATAGCCTGGCAGTCCG 1140
Db |||||
QY 1081 CTGCATCACCCATCAGAGAGGGGAAAGATTTCTGCAAAATGAGAAATAGCCTGGCAGTCCG 1140
Db |||||
QY 1141 TTCACCCCTGCCGAAAGATGACTCCCGTGACTCCCGAGTAAAGAGTGAAGTGAAGTTCGAGTCCG 1200
Db |||||
QY 1141 TTCACCCCTGCCGAAAGATGACTCCCGTGACTCCCGAGTAAAGAGTGAAGTTCGAGTCCG 1200
Db |||||
QY 1201 TGTCCATTCACAGCCACTAAGTCCAGATTCAGAGCCTCCAGTCTTTCTGAAAAGTCTCC 1260
Db |||||
QY 1201 TGTCCATTCACAGCCACTAAGTCCAGATTCAGAGCCTCCAGTCTTTCTGAAAAGTCTCC 1260
Db |||||
QY 1261 TCCCAAGCAATGAAGAGTTTCAGGCCTCTGCAAGAGAGACTGCGTGGAAATGTGAGAA 1320
Db |||||
QY 1261 TCCCAAGCAATGAAGAGTTTCAGGCCTCTGCAAGAGAGACTGCGTGGAAATGTGAGAA 1320
Db |||||
QY 1321 GACAGTCTATCCAAATGGAGCGTCTTGGCCCAACAGCAGAGTGTTCACATCAGCTGCTT 1380
Db |||||
QY 1321 GACAGTCTATCCAAATGGAGCGTCTTGGCCCAACAGCAGAGTGTTCACATCAGCTGCTT 1380
Db |||||
QY 1381 CGTTGCTCTTATGCAACAACAACTCAGTCTAGAACATATGCATCTTTACATGGRAG 1440
Db |||||
QY 1381 CGTTGCTCTTATGCAACAACAACTCAGTCTAGAACATATGCATCTTTACATGGRAG 1440
Db |||||
QY 1441 AATCTATTGTAAGCCTCACTTCAATCAACTCTTTTAAATCTTAAGGGCAACTATGATGAAG 1500
Db |||||
QY 1441 AATCTATTGTAAGCCTCACTTCAATCAACTCTTTTAAATCTTAAGGGCAACTATGATGAAG 1500
Db |||||
QY 1501 CTTTGGGCACACACACAGGATCTATGGGCAAGCAAAATGAAAAACGAGAGATTTT 1560
Db |||||
QY 1501 CTTTGGGCACACACACAGGATCTATGGGCAAGCAAAATGAAAAACGAGAGATTTT 1560
Db |||||
QY 1561 GGAGAGACAGCCCGAGCTTGCAAAATGCAAGGAGACCCCTCACAGCCCGGGGTAGAAGA 1620
Db |||||
QY 1561 GGAGAGACAGCCCGAGCTTGCAAAATGCAAGGAGACCCCTCACAGCCCGGGGTAGAAGA 1620
Db |||||

QY 1621 TGCCCTATTGCTAAGGTGGGTGCTCGCTGCAAGTATGGAAGCAAGGCGCTCCTCTCA 1680
Db 1621 TGCCCTATTGCTAAGGTGGGTGCTCGCTGCAAGTATGGAAGCAAGGCGCTCCTCTCA 1680
QY 1681 GCAGGAGGAAGCAAGCCAGCTGAAACCAAGAGCTGAGGATCGCCTCGCCACCCCC 1740
Db 1681 GCAGGAGGAAGCAAGCCAGCTGAAACCAAGAGCTGAGGATCGCCTCGCCACCCCC 1740
QY 1741 CACTGAACCTTGAAGTTCAGGAAGTGCCTTGGAAGAGGGATCAAAATGTCAAAAGCCCAA 1800
Db 1741 CACTGAACCTTGAAGTTCAGGAAGTGCCTTGGAAGAGGGATCAAAATGTCAAAAGCCCAA 1800
QY 1801 ATGGCCCTCTGAAGACGAATCAGCAAGCCCGAAGTTCCTGAGGATGCGATCTAGATCT 1860
Db 1801 ATGGCCCTCTGAAGACGAATCAGCAAGCCCGAAGTTCCTGAGGATGCGATCTAGATCT 1860
QY 1861 GAAGAAGCTAAGACGATCTTCTCACTGAAGGAAGAGCCGCCAATTCAGTGTAGCAGC 1920
Db 1861 GAAGAAGCTAAGACGATCTTCTCACTGAAGGAAGAGCCGCCAATTCAGTGTAGCAGC 1920
QY 1921 TTCATTTCAAAGCACCTCTGTCAAGAGCCCAAAACCTGTGTCCCACTCTATCAGGAAGG 1980
Db 1921 TTCATTTCAAAGCACCTCTGTCAAGAGCCCAAAACCTGTGTCCCACTCTATCAGGAAGG 1980
QY 1981 CTGGAGCATGTCAGAGCAGAGTGAAGAGTCTGTGGTGGAGAGTTGCAGAAAGGAACA 2040
Db 1981 CTGGAGCATGTCAGAGCAGAGTGAAGAGTCTGTGGTGGAGAGTTGCAGAAAGGAACA 2040
QY 2041 AGTGGAAATGCCAAGCTCTCTAGAGAGATGGAATGTGGGAAACCAACCTGGCAAAA 2100
Db 2041 AGTGGAAATGCCAAGCTCTCTAGAGAGATGGAATGTGGGAAACCAACCTGGCAAAA 2100
QY 2101 CAAAGAACTCTAAGGAGAGACAGGAAGAGTAAGGAAGGTCATAGTTTGAGATGGA 2160
Db 2101 CAAAGAACTCTAAGGAGAGACAGGAAGAGTAAGGAAGGTCATAGTTTGAGATGGA 2160
QY 2161 GAATGAGAACTCTGTGAAATGGTGAGACTCCGATGAAGATGATAACAGCTTCTCTCAA 2220
Db 2161 GAATGAGAACTCTGTGAAATGGTGAGACTCCGATGAAGATGATAACAGCTTCTCTCAA 2220
QY 2221 ACAACATCTCCACAGAACCCCAAGTCTCTGAATTTGGTGGAGTTTGTAGACAAACCTT 2280
Db 2221 ACAACATCTCCACAGAACCCCAAGTCTCTGAATTTGGTGGAGTTTGTAGACAAACCTT 2280
QY 2281 TGCTGAAGAATTCACCTACTCAGAAATCAGAAATCCAGAGTGTGGAACTCTGGAGGGAGA 2340
Db 2281 TGCTGAAGAATTCACCTACTCAGAAATCAGAAATCCAGAGTGTGGAACTCTGGAGGGAGA 2340
QY 2341 AGTGTCAAAGAGCTCTCTGTGGAAGAACAGATAAAGAGAAATCGGTATTTATGATCAGGA 2400
Db 2341 AGTGTCAAAGAGCTCTCTGTGGAAGAACAGATAAAGAGAAATCGGTATTTATGATCAGGA 2400
QY 2401 TGAGGATGAAGAGTGACAAATTTGCAATGATGTGGGCCCTTAAATTCATGTTAGTGTAGC 2460
Db 2401 TGAGGATGAAGAGTGACAAATTTGCAATGATGTGGGCCCTTAAATTCATGTTAGTGTAGC 2460
QY 2461 GAGCCACTGCCCTTTGTGCAAAATGTGATCCACATGAAGAGTATCCAGCATGAAATGTA 2520
Db 2461 GAGCCACTGCCCTTTGTGCAAAATGTGATCCACATGAAGAGTATCCAGCATGAAATGTA 2520
QY 2521 ATTTACTTGGAAAGTAACTTTGGAAGAAATTCCTTCTTAAATCAAAACCAAAACAAAA 2580
Db 2521 ATTTACTTGGAAAGTAACTTTGGAAGAAATTCCTTCTTAAATCAAAACCAAAACAAAA 2580
QY 2581 AACACAAAAACACATTTCTAAATCTAGAGATAACTTTACTTAAATCTTCAATTTAGCA 2640
Db 2581 AACACAAAAACACATTTCTAAATCTAGAGATAACTTTACTTAAATCTTCAATTTAGCA 2640
QY 2641 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2700
Db 2641 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2700
QY 2701 GCCCAGATTCTACTGTATTCCCAAGGCAATATTAAAGGTAGATAGTATTAGTAGTAT 2760

Db 2701 GCCCAGATTCTACTGTATTCCCAAGGCAATATTAAAGGTAGATAGTATTAGTAGTAT 2760
QY 2761 ATTGTTACACACTATTTTTGAATTTAGAGAACATACAGAGGAATTTAGGGGCTTTAAACAT 2820
Db 2761 ATTGTTACACACTATTTTGGAATTTAGAGAACATACAGAGGAATTTAGGGGCTTTAAACAT 2820
QY 2821 TAGACTGAATGCACCTTTAGTATAAAGGGCACAGTTTGTATATTTTAAATGAATACCAA 2880
Db 2821 TAGACTGAATGCACCTTTAGTATAAAGGGCACAGTTTGTATATTTTAAATGAATACCAA 2880
QY 2881 TTTAAATTTTGTAGTATTACCTGTTAAGAGATTTTGTAGTCTTTAAATTTTGTAGTTAA 2940
Db 2881 TTTAAATTTTGTAGTATTACCTGTTAAGAGATTTTGTAGTCTTTAAATTTTGTAGTTAA 2940
QY 2941 TTTTCTTGCTGTGATATATATGAGGAATTTACTACTTTATGTCTCTCTAAACCTACA 3000
Db 2941 TTTTCTTGCTGTGATATATATGAGGAATTTACTACTTTATGTCTCTCTAAACCTACA 3000
QY 3001 TCTGAACCTCGAGCTCTCGGTGCTTAGAGAGATCTGTGCTCCCAATAAGCTTTTGTATC 3120
Db 3001 TCTGAACCTCGAGCTCTCGGTGCTTAGAGAGATCTGTGCTCCCAATAAGCTTTTGTATC 3120
QY 3061 CGAACCTACACTCTTCGGTGTCTTAGAGAGATCTGTGCTCCCAATAAGCTTTTGTATC 3120
Db 3061 CGAACCTACACTCTTCGGTGTCTTAGAGAGATCTGTGCTCCCAATAAGCTTTTGTATC 3120
QY 3121 TGCCAGTGAATTTACTGTACTCCAAATGATTCCTTTCTTTCTGTGTATCTGTGCTTC 3180
Db 3121 TGCCAGTGAATTTACTGTACTCCAAATGATTCCTTTCTTTCTGTGTATCTGTGCTTC 3180
QY 3181 TCATAATTACTGAAAGCTGCAATATTTTAGTAATACCTTCGGGATCAGTGTCCCCATCT 3240
Db 3181 TCATAATTACTGAAAGCTGCAATATTTTAGTAATACCTTCGGGATCAGTGTCCCCATCT 3240
QY 3241 TCCGTGTTAGAGCAAGTGAAGAGTTTAAAGGAGGAAGAAAGAACTGTCTTACACCA 3300
Db 3241 TCCGTGTTAGAGCAAGTGAAGAGTTTAAAGGAGGAAGAAAGAACTGTCTTACACCA 3300
QY 3301 CTGGAGCTCAGACCTCTAAACCCCTGTATTTCCCTTATGATGTCCCTTTTGTAGACACTA 3360
Db 3301 CTGGAGCTCAGACCTCTAAACCCCTGTATTTCCCTTATGATGTCCCTTTTGTAGACACTA 3360
QY 3361 ATTTTAAATACTTACTAGCTCTGAAATATATTTGATTTTATCAGATATTTCTCAGGGTG 3420
Db 3361 ATTTTAAATACTTACTAGCTCTGAAATATATTTGATTTTATCAGATATTTCTCAGGGTG 3420
QY 3421 AAATTAACCAACTATAGGCCCTTTTCTTGGGATGATTTTCTAGTCTTAAAGGTTTGGGA 3480
Db 3421 AAATTAACCAACTATAGGCCCTTTTCTTGGGATGATTTTCTAGTCTTAAAGGTTTGGGA 3480
QY 3481 CATTTAAACCTTGAGTACATTTGTTGTACACAGTTGATATTTCCAAATTTGTATGGATGGA 3540
Db 3481 CATTTAAACCTTGAGTACATTTGTTGTACACAGTTGATATTTCCAAATTTGTATGGATGGA 3540
QY 3541 GGGAGAGGTGCTTTAAGCTGTAGGCTTTTCTTGTACTGCAATTTATAGAGATTTAGCTTT 3600
Db 3541 GGGAGAGGTGCTTTAAGCTGTAGGCTTTTCTTGTACTGCAATTTATAGAGATTTAGCTTT 3600
QY 3601 AATATTTTTTAGAGATGATAAACAATCTGCTTTCTTGTACTGCAATTTATAGAGATTTAGCTTT 3660
Db 3601 AATATTTTTTAGAGATGATAAACAATCTGCTTTCTTGTACTGCAATTTATAGAGATTTAGCTTT 3660
QY 3661 TTATTCATTAAGATTTTAAATTTAAATTTGAAAAAATAAAAAA 3705
Db 3661 TTATTCATTAAGATTTTAAATTTAAATTTGAAAAAATAAAAAA 3705

RESULT 2

ABX71307

ID ABX71307 standard; cDNA; 3664 BP.

XX

AC ABX71307;

XX
DT 14-APR-2003 (first entry)
XX
DE Human transcription factor cDNA from clone DKFZphutcl_18c19.
XX
KW Human; gene; Gene therapy; vaccine; disease treatment; detection; ss.
XX
OS Homo sapiens.
XX
PN W0200112659-A2.
XX
PD 22-FEB-2001.
XX
PE 18-AUG-2000; 2000WO-1B01496.
XX
PR 18-AUG-1999; 99US-0149499.
PR 28-SEP-1999; 99US-0156503.
XX
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX
PI Wiemann S;
XX
DR WPI; 2001-327840/34.
DR P-PSDB; ABU52869.
XX
PT Nucleic acids having the sequences of clones isolated from libraries of
PT different human tissues, useful in recombinant DNA methodologies -
XX
PS Claim 1; Page 449-450; 1093pp; English.
XX
CC This invention describes novel polynucleotides and polypeptides isolated
CC from human cDNA libraries which can be used for gene therapy or in
CC vaccines. The polynucleotides of the invention and antibodies encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The products of the
CC invention may also be used to identify modulators of expression and
CC activity and to down regulate expression and activity. The antibodies of
CC the invention may also be used as diagnostic agents for detecting the
CC presence of polypeptides in samples. This sequence encodes a polypeptide
CC described in the disclosure of the invention.
XX
SQ Sequence 3664 BP; 1210 A; 734 C; 809 G; 911 T; 0 other;

Query Match 97.5%; Score 3611; DB 23; Length 3664;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3661; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 44 GCGCTAGGTAGCGCGCGGACCTGTGACAGGGCTGGTAGCGCGCAGAGGAAGCGGC 103
DB 1 GCGCTAGGTAGCGCGCGGACCTGTGACAGGGCTGGTAGCGCGCAGAGGAAGCGGC 60
QY 104 TTTTAGCCAGGTATTTTCAAGTGTCTGTAGACAGATGGAATCATCTCCATTTAATAGCGG 163
DB 61 TTTTAGCCAGGTATTTTCAAGTGTCTGTAGACAGATGGAATCATCTCCATTTAATAGCGG 120
QY 164 CAATGSGACCTCACTATCAATGAGGGTAACAGCCAAAGAACTTTCTTGTGTCAACAAGAAC 223
DB 121 CAATGSGACCTCACTATCAATGAGGGTAACAGCCAAAGAACTTTCTTGTGTCAACAAGAAC 180
QY 224 AAGTCATCGGCTATTTGGGAAATATTTCCAAAGTACAGAAAGACAGCTGAAGAAACAAAC 283
DB 181 AAGTCATCGGCTATTTGGGAAATATTTCCAAAGTACAGAAAGACAGCTGAAGAAACAAAC 240
QY 284 ATGGAGAAGAGAGAGTACACCGGAAATCTTCCAGCACTTTAGAAAGGGGACCCCTG 343
DB 241 ATGGAGAAGAGAGAGTACACCGGAAATCTTCCAGCACTTTAGAAAGGGGACCCCTG 300
QY 344 ACTGTGTTAAAGAGAGTGGGAGAACCCAGGGCTGGGACGAGTCTCACACAGACTCT 403
DB 301 ACTGTGTTAAAGAGAGTGGGAGAACCCAGGGCTGGGACGAGTCTCACACAGACTCT 360
QY 404 CTACGGAACAGCAGCACTGAGATTAGGSCACAGAGCAGACCATCTCTCTCTGAGTGACA 463
DB |||||

DB 361 CTACGGAACAGCAGCACTGAGATTAGGCACAGACGACCATCTCTCTGCTGAAAGTGACA 420
QY 464 AGCCACGCTGTTCTGGAGCCAAAGCTGACCAAGAGAAACAAATCCACCTCCAGATCTAGA 523
DB 421 AGCCACGCTGTTCTGGAGCCAAAGCTGACCAAGAGAAACAAATCCACCTCCAGATCTAGA 480
QY 524 CTCAGGTACCTCTCTGAAGCCCTGTTTCAAGGTGATATCCCCACATCAAGAGCGGTGAG 583
DB 481 CTCAGGTACCTCTCTGAAGCCCTGTTTCAAGGTGATATCCCCACATCAAGAGCGGTGAG 540
QY 584 GATCTTAAAGACCACCTCAACAGAGAAAGTAAAGAAATGAAATTTGTTAGAGAAATCCAGG 643
DB 541 GATCTTAAAGACCACCTCAACAGAGAAAGTAAAGAAATGAAATTTGTTAGAGAAATCCAGG 600
QY 644 CATGAAGTAGAAAAATCAGAAATCAGTGAACACACAGATGCTTCGGGCAAAATAGAGAAA 703
DB 601 CATGAAGTAGAAAAATCAGAAATCAGTGAACACACAGATGCTTCGGGCAAAATAGAGAAA 660
QY 704 TATAATGTTCCGTGAACAGGCTTAAGATGATGTTTGAAGAAAGTGAACCAATCAAACT 763
DB 661 TATAATGTTCCGTGAACAGGCTTAAGATGATGTTTGAAGAAAGTGAACCAATCAAACT 720
QY 764 AAGATTCCTCGGGCCCAAGCCGAAAGTGAAGTGAAGGAAGATCTCTGAAAAACAGCTAT 823
DB 721 AAGATTCCTCGGGCCCAAGCCGAAAGTGAAGTGAAGGAAGATCTCTGAAAAACAGCTAT 780
QY 824 TCTCTAGATCACTTGGAAATAGCCCGAGGTGCTGTCATCTTCTACATTTGACTCGGAG 893
DB 781 TCTCTAGATCACTTGGAAATAGCCCGAGGTGCTGTCATCTTCTACATTTGACTCGGAG 840
QY 884 AAAAAATGAGAGTAGAGCAAAATCTGAACTTCCACGCTCTCAGAAACCTCTATTAAGGAT 943
DB 841 AAAAAATGAGAGTAGAGCAAAATCTGAACTTCCACGCTCTCAGAAACCTCTATTAAGGAT 900
QY 944 CGAATGCGCAAGTACAGGAGCTGTGTCCAAACAAAGCAGCTCAACCAACTATACAAAT 1003
DB 901 CGAATGCGCAAGTACAGGAGCTGTGTCCAAACAAAGCAGCTCAACCAACTATACAAAT 960
QY 1004 GAGCTCAAAAGCCAGTGTGTCGCAAAATCAAAATTCATAAAATGGAGCAAAAGAGAAATGTG 1063
DB 961 GAGCTCAAAAGCCAGTGTGTCGCAAAATCAAAATTCATAAAATGGAGCAAAAGAGAAATGTG 1020
QY 1064 CCCCCAGGTCCTGAGGTCTGCAATCAACCCATCAGGAAGGGGAAAGATTTCTCCAAATGAG 1123
DB 1021 CCCCCAGGTCCTGAGGTCTGCAATCAACCCATCAGGAAGGGGAAAGATTTCTCCAAATGAG 1080
QY 1124 AATAGCCTGGCAGTCTGTTCCACCCCTCCCGAAGATGACTCCCGTGACTCCCGAGGTTAAG 1183
DB 1081 AATAGCCTGGCAGTCTGTTCCACCCCTCCCGAAGATGACTCCCGTGACTCCCGAGGTTAAG 1140
QY 1184 AGTGAGGTTCAACAGCCTGTCCATCCCAAGCCACTAAGTCCAGATTCAGAGCCTCCAGT 1243
DB 1141 AGTGAGGTTCAACAGCCTGTCCATCCCAAGCCACTAAGTCCAGATTCAGAGCCTCCAGT 1200
QY 1244 CTTTCTGAAAGTTCTCTCCCAAGCAATGAAGAGTTTCAGGCACCTGCAAGAGAGACC 1303
DB 1201 CTTTCTGAAAGTTCTCTCCCAAGCAATGAAGAGTTTCAGGCACCTGCAAGAGAGACC 1260
QY 1304 TCGGTGGAATTCAGAGACAGTCTATCCATGAGAGGCTCTTGGCCCAACCCAGAGG 1363
DB 1261 TCGGTGGAATTCAGAGACAGTCTATCCATGAGAGGCTCTTGGCCCAACCCAGAGG 1320
QY 1364 TTTTCAATCAGCTGCTCCGTTGCTCTTATTCGAACCAACAACTCAGTCTAGGAACATAT 1423
DB 1321 TTTTCAATCAGCTGCTCCGTTGCTCTTATTCGAACCAACAACTCAGTCTAGGAACATAT 1380
QY 1424 GCATCTTTTACATGAAGAACTATTTAGGCTCACTTTCAATCAACTCTTTTAAATCTTAAG 1483
DB 1391 GCATCTTTTACATGAAGAACTATTTAGGCTCACTTTCAATCAACTCTTTTAAATCTTAAG 1440
QY 1484 GGCAACTATGATGAAGGCTTTGGGCACAGACACAGAGGATCTATGGGCAAGCAAAAAT 1543
DB 1441 GGCAACTATGATGAAGGCTTTGGGCACAGACACAGAGGATCTATGGGCAAGCAAAAAT 1500

QY 1544 GAAACGAAAGAGATTTTGGAGAGACAGCCAGCTTGCATAATGCAAGGGAGAGACCCCTCAC 1603
DB 1501 GAAACGAAAGAGATTTTGGAGAGACAGCCAGCTTGCATAATGCAAGGGAGAGACCCCTCAC 1560
QY 1604 AGCCAGGGGTAGAGATGCGCCCTATTGCTAGAGTGGGTGCTCTGGCTGCAAGTATGAA 1663
DB 1561 AGCCAGGGGTAGAGATGCGCCCTATTGCTAGAGTGGGTGCTCTGGCTGCAAGTATGAA 1620
QY 1664 GCCAAGGCTCTCTCAGCAGAGAGAGAGCAAGCCAGCTGAAACCAAGAGCTGAGG 1723
DB 1621 GCCAAGGCTCTCTCAGCAGAGAGAGAGCAAGCCAGCTGAAACCAAGAGCTGAGG 1680
QY 1724 ATCGGCTGGCCACCCCTCACTGAACTTGGAAAGTTCAGGAAGTGCCTTGGAGGAAGGATC 1783
DB 1681 ATCGGCTGGCCACCCCTCACTGAACTTGGAAAGTTCAGGAAGTGCCTTGGAGGAAGGATC 1740
QY 1784 AAAATGTCAAAGCCCAATGGCTCTCAAGAGCAAAATCAGCAAGCCCGAAGTTCCTGAG 1843
DB 1741 AAAATGTCAAAGCCCAATGGCTCTCAAGAGCAAAATCAGCAAGCCCGAAGTTCCTGAG 1800
QY 1844 GATGTCGATCTAGATCTGAAGAGCTAAGACGATCTTCAAGAGCACCTCTGTCAAGAGCCCAAAACCTGTGTC 1903
DB 1801 GATGTCGATCTAGATCTGAAGAGCTAAGACGATCTTCAAGAGCACCTCTGTCAAGAGCCCAAAACCTGTGTC 1860
QY 1904 CCATTCACTGTAGCAGCTTCAATTTCAAAGCACCTCTGTCAAGAGCCCAAAACCTGTGTC 1963
DB 1861 CCATTCACTGTAGCAGCTTCAATTTCAAAGCACCTCTGTCAAGAGCCCAAAACCTGTGTC 1920
QY 1964 CCACCTATCAGGAAGGCTGGAGCATGTGAGCAGAGTGAAGAGTCTGTGGGTGGAAGA 2023
DB 1921 CCACCTATCAGGAAGGCTGGAGCATGTGAGCAGAGTGAAGAGTCTGTGGGTGGAAGA 1980
QY 2024 GTTGAGAAAGGAACCAAGTGGAAATCTTAAGAGAGACAGGAGAGAGTGAAGAGT 2083
DB 1981 GTTGAGAAAGGAACCAAGTGGAAATCTTAAGAGAGACAGGAGAGAGTGAAGAGT 2040
QY 2084 AAAACAACCTGGCAAAACAAAGATCTTAAGAGAGACAGGAGAGAGTGAAGAGT 2143
DB 2041 AAAACAACCTGGCAAAACAAAGATCTTAAGAGAGACAGGAGAGAGTGAAGAGT 2100
QY 2144 CATAGTTGGAGTGGAGATGAGAACTCTGTGAGAAATGGTGCAGACTCCGATGAAGAT 2203
DB 2101 CATAGTTGGAGTGGAGATGAGAACTCTGTGAGAAATGGTGCAGACTCCGATGAAGAT 2160
QY 2204 GATAACAGCTCTCTCAACACCAATCTCCAGAGACAGGAGAGAGTCTCTGAATTCGTCAGT 2263
DB 2161 GATAACAGCTCTCTCAACACCAATCTCCAGAGACAGGAGAGAGTCTCTGAATTCGTCAGT 2220
QY 2264 TTTGTAGACAACACCTTTGCTGAAGAACTCACTACTCAGAAATCCCAAGTCTCTGAATTCGTCAGT 2323
DB 2221 TTTGTAGACAACACCTTTGCTGAAGAACTCACTACTCAGAAATCCCAAGTCTCTGAATTCGTCAGT 2280
QY 2324 GAACTCTGGGAGGAGAGTGGTCAAGAGCTCTCTGTGGAAGAACAGATATAAGAGAAAT 2383
DB 2281 GAACTCTGGGAGGAGAGTGGTCAAGAGCTCTCTGTGGAAGAACAGATATAAGAGAAAT 2340
QY 2384 CGGTATTATGATGAGGATGAGGATGAGAGTGCAAAATGCAATGATGCTGGGCTTAAA 2443
DB 2341 CGGTATTATGATGAGGATGAGGATGAGAGTGCAAAATGCAATGATGCTGGGCTTAAA 2400
QY 2444 TTTGATGTTAGTGTAGCGGCCACTGCCCTTTGTCAAAATGTCATGTCACATTAAGCAGGTA 2503
DB 2401 TTTGATGTTAGTGTAGCGGCCACTGCCCTTTGTCAAAATGTCATGTCACATTAAGCAGGTA 2460
QY 2504 TCCCAGATGAAATGTAATTTACTTGGAAAGTAACTTTGGAAGAAATTCCTTCTTAAAT 2563
DB 2461 TCCCAGATGAAATGTAATTTACTTGGAAAGTAACTTTGGAAGAAATTCCTTCTTAAAT 2520
QY 2564 CAAAAACAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAAAC 2623
DB 2521 CAAAAACAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAAAC 2580

QY 2624 AATTCCTTCATTTTAGCAGTGATGATATGCATAAGTCTGTAAAGCTTGTAACTGGGAAA 2683
DB 2581 AATTCCTTCATTTTAGCAGTGATGATATGCATAAGTCTGTAAAGCTTGTAACTGGGAAA 2640
QY 2684 TATTCACCTGATTAATAGCCAGATCTCTACTGTAATCCCAAAAGCAATATTAAGGTAGA 2743
DB 2641 TATTCACCTGATTAATAGCCAGATCTCTACTGTAATCCCAAAAGCAATATTAAGGTAGA 2700
QY 2744 TAGATGATTAGTAGTATTAATTTTACACACTATTTTGAATTTAGAGAACATACAGAAAGAA 2803
DB 2701 TAGATGATTAGTAGTATTAATTTTACACACTATTTTGAATTTAGAGAACATACAGAAAGAA 2760
QY 2804 TTTAGGGGCTTAAACATTAGACTGAATGCACCTTTAGTATAAAGGGCAGAGTTTGTATAT 2863
DB 2761 TTTAGGGGCTTAAACATTAGACTGAATGCACCTTTAGTATAAAGGGCAGAGTTTGTATAT 2820
QY 2864 TTTTAAATGAATACCAATTTAATTTTGTATTTTACCTGTTAAGAGATTAATTTAGTCTT 2923
DB 2821 TTTTAAATGAATACCAATTTAATTTTGTATTTTACCTGTTAAGAGATTAATTTAGTCTT 2880
QY 2924 TAAATTTTGTAGTTAATTTTCTGTGTGATATATATGAGGAATTTACTACTTTATGTC 2983
DB 2881 TAAATTTTGTAGTTAATTTTCTGTGTGATATATATGAGGAATTTACTACTTTATGTC 2940
QY 2984 CTGCTCTTAAACTACATCTGAACTCGAGCTCGAGGTATAATACACAGAGCACTTT 3043
DB 2941 CTGCTCTTAAACTACATCTGAACTCGAGCTCGAGGTATAATACACAGAGCACTTT 3000
QY 3044 TTGAGGCAATTTGAAAACCAACCTACACTCTTGGGTCTTAGAGAGATCTGCTGTCTCC 3103
DB 3001 TTGAGGCAATTTGAAAACCAACCTACACTCTTGGGTCTTAGAGAGATCTGCTGTCTCC 3060
QY 3104 AAATAAGCTTTTGTATCTGCGAGTGAATTTACTGTAATCTGTAATCTGTAATCTGTTCT 3163
DB 3061 AAATAAGCTTTTGTATCTGCGAGTGAATTTACTGTAATCTGTAATCTGTTCTGTTCT 3120
QY 3164 GGTGATATCTGCTTCTCTCATTAATTTACTGAAAGCTGCAATATTTTAGTAATACCTTCGG 3223
DB 3121 GGTGATATCTGCTTCTCTCATTAATTTACTGAAAGCTGCAATATTTTAGTAATACCTTCGG 3180
QY 3224 ATCACTGTCTCCCATCTTCCGTGTTAGAGCAAGTGAAGAGTTTAAAGGAGAAAGAA 3283
DB 3181 ATCACTGTCTCCCATCTTCCGTGTTAGAGCAAGTGAAGAGTTTAAAGGAGAAAGAA 3240
QY 3284 AGAAGCTCTTACACACTTTGAGCTCAGACCTCTTAAACCTGTATTTCCCTTATGATGTC 3343
DB 3241 AGAAGCTCTTACACACTTTGAGCTCAGACCTCTTAAACCTGTATTTCCCTTATGATGTC 3300
QY 3344 CCCTTTTGGAGACACTAATTTTAAATACTTACTGAGCTTAAACCTGTATTTCCCTTATGATGTC 3403
DB 3301 CCCTTTTGGAGACACTAATTTTAAATACTTACTGAGCTTAAACCTGTATTTAGTATGTC 3360
QY 3404 ACAGTATCTCAGGTGAAATTTAAACCAACTATAGGCTTTTCTTGGGATGATTTCTTA 3463
DB 3361 ACAGTATCTCAGGTGAAATTTAAACCAACTATAGGCTTTTCTTGGGATGATTTCTTA 3420
QY 3464 GTCCTTAAAGTTTGGGACATTTAAACCTTGAAGTACATTTGTTGACACAGTGTATTTCC 3523
DB 3421 GTCCTTAAAGTTTGGGACATTTAAACCTTGAAGTACATTTGTTGACACAGTGTATTTCC 3480
QY 3524 AAATTTGATGATGGAGGAGAGGCTCTTAAGCTGAGGCTTTTCTTGTACTGCAAT 3583
DB 3481 AAATTTGATGATGGAGGAGAGGCTCTTAAGCTGAGGCTTTTCTTGTACTGCAAT 3540
QY 3584 TATAGAGATTTAGCTTTAATTTTGTAGAGATGTAAGCAATCTGCTTCTTACTGCTTA 3643
DB 3541 TATAGAGATTTAGCTTTAATTTTGTAGAGATGTAAGCAATCTGCTTCTTACTGCTTA 3600
QY 3644 CCTAGCTGAAACATTTTATCAATAAGATTTTAAATTTAAATTTTCAAAAAA 3703
DB 3601 CCTAGCTGAAACATTTTATTTCAATAAGATTTTAAATTTAAATTTTCAAAAAA 3660
QY 3704 AA 3705

Db 3661 AA 3662
RESULT 3
AAC77143
ID AAC77143 standard; cDNA; 3711 BP.
XX AC AAC77143;
XX XX
DT 08-FEB-2001 (first entry)
XX XX
DE Human ORFX ORF2698 polynucleotide sequence SEQ ID NO:5395.
XX XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnary; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive; ss.
XX XX
OS Homo sapiens.
XX XX
PN WO200058473-A2.
XX XX
PD 05-OCT-2000.
XX XX
PF 31-MAR-2000; 2000MO-US08621.
XX XX
PR 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX XX
PA (CURA-) CURAGEN CORP.
XX XX
PI Shimkets RA, Leach M;
XX XX
DR WPI: 2000-602362/57.
XX XX
PT P-PSDB; AAB42934.
XX XX
PT Novel nucleic acids and peptides derived from open reading frame X,
XX XX
PS useful for treating e.g. cancers, proliferative disorders,
XX XX
PS neurodegenerative disorders and cardiovascular disease -
XX XX
PS Claim 5; Page 4578-4580; 5507pp; English.
XX XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
CC antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; coagulant; vasotropic;
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antithyroid; and antianaemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder.
CC The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC

CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX XX
SQ Sequence 3711 BP; 1215 A; 747 C; 830 G; 919 T; 0 other;
Query Match 92.1%; Score 3412; DB 21; Length 3711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3702; Conservative 0; Mismatches 1; Indels 3; Gaps 1;
QY 1 GGCGCAGGACGACGAGTGGTGTAGCAGCTTGGTCGCACAGGTGCGGTAGGTAGAGCGCC 60
DB 6 GGCGCGCAGGACGAGTGGTGTAGCAGCTTGGTCGCACAGGTGCGGTAGGTAGAGCGCC 65
QY 61 GGGACCTGTGACAGGGCTGGTAGCAGCGCAGAGAAAGGGCGCTTTTAGCCAGGTATTTC 120
DB 66 GGGACCTGTGACAGGGCTGGTAGCAGCGCAGAGAAAGGGCGCTTTTAGCCAGGTATTTC 125
QY 121 AGTGTCTGTAGACAAAGATGGAATCATCTCCATTTAATAGACGGCAATGGACCTCAGCTATC 180
DB 126 AGTGTCTGTAGACAGGATGGAATCATCTCCATTTAATAGACGGCAATGGACCTCAGCTATC 185
QY 181 ATTGAGGTACACCCAAAGAACTTCTCTGTCAACAAGAAAGTCAATCGGCTATTGT 240
DB 186 ATTGAGGTAAACAGCCAAAGAACTTCTCTGTCAACAAGAAAGTCAATCGGCTATTGT 245
QY 241 GGAATAATTCTCAAGTACAGAAAGCAGCTGAAGAAACAAACATGGAGAAGAGAGAG 300
DB 246 GGAATAATTCTCAAGTACAGAAAGCAGCTGAAGAAACAAACATGGAGAAGAGAGAG 305
QY 301 TAACACCGAAATCTCTCCAGCACTTTAGAAAGGGGACCCCTGACTGTGTAAAGAGAA 360
DB 306 TAACACCGAAATCTCTCCAGCACTTTAGAAAGGGGACCCCTGACTGTGTAAAGAGAA 365
QY 361 GTGGAGAACCCAGGGCTGGGACGAGTCTCACACAGACTCTCTACGGAAACAGCAGCAC 420
DB 366 GTGGAGAACCCAGGGCTGGGACGAGTCTCACACAGACTCTCTACGGAAACAGCAGCAC 425
QY 421 TGAGATTAGCAGCAGACGACCATCTCTCTGTGAAGTGAAGCAAGCCAGCTCTCTGG 480
DB 426 TGAGATTAGCAGCAGACGACCATCTCTCTGTGAAGTGAAGCAAGCCAGCTCTCTGG 485
QY 481 AGCCAAAGCTGACCAAGAAAGCAAAATCCACCCAGATCTAGACTCAGGTCACTCTGA 540
DB 486 AGCCAAAGCTGACCAAGAAAGCAAAATCCACCCAGATCTAGACTCAGGTCACTCTGA 545
QY 541 AGCCCTCGTTAGGGTTCGATATCCCCACATCAAGGACGGTGAGGATCTTAAAGACCACTC 600
DB 546 AGCCCTCGTTAGGGTTCGATATCCCCACATCAAGGACGGTGAGGATCTTAAAGACCACTC 605
QY 601 AACAGAAAGTAAAAAATGGAAAAATTTGTCTAGGAGAAATCCAGGCATGAAAGTAAAAATC 660
DB 606 AACAGAAAGTAAAAAATGGAAAAATTTGTCTAGGAGAAATCCAGGCATGAAAGTAAAAATC 665
QY 661 AGAAATCAAGTAAAAACACAGATGCTTCGGGCAAAATAGAGAAATATAATGTTCCTGAA 720
DB 666 AGAAATCAAGTAAAAACACAGATGCTTCGGGCAAAATAGAGAAATATAATGTTCCTGAA 725
QY 721 CAGGCTTAAGATGATGTTTGAAGAAAGTGACCAACTCAAACTAGATCTCCGGGCCCA 780
DB 726 CAGGCTTAAGATGATGTTTGAAGAAAGTGACCAACTCAAACTAGATCTCCGGGCCCA 785
QY 781 AAGCCGAAGTCAAGTGAAGGAGAGATCTCTGAAACAGCTATTCTCTAGATGACCTGGA 840
DB 786 AAGCCGAAGTCAAGTGAAGGAGAGATCTCTGAAACAGCTATTCTCTAGATGACCTGGA 845
QY 841 AATAGGCCAGGTAGTGTCTATCTTACATTTGACTCGGAGAAAAATGAGATGACG 900
DB 846 AATAGGCCAGGTAGTGTCTATCTTACATTTGACTCGGAGAAAAATGAGATGACG 905
QY 901 AAATCTGGAATCTCCAGCCCTCTCAGAAACCTCTATAAGGATCGAATGCCCAAGTACCA 960
DB 906 AAATCTGGAATCTCCAGCCCTCTCAGAAACCTCTATAAGGATCGAATGCCCAAGTACCA 965

Db 3126 ATCTGCCAGTGAATTTACTGTACTCCAAATGATTGCTTTCTTCGGTGATATCTGTGC 3185
QY TTCTCATAATTACTGAAAGCTCAATATTTTAGTAATACCTTCGGGATCACTGTCCCCCA 3237
Db TTCTCATAATTACTGAAAGCTCAATATTTTAGTAATACCTTCGGGATCACTGTCCCCCA 3245
QY TCTTCCGTGTTAGAGCAAAAGTGAAGAGTTTAAAGGAGGAGAAAGAAAGTCTTTACA 3297
Db TCTTCCGTGTTAGAGCAAAAGTGAAGAGTTTAAAGGAGGAGAAAGAAAGTCTTTACA 3305
QY CCACTTGAGCTCAGACCTCTAAACCCGTATTTCCCTTATGATGTCCTTTTTCGAGACA 3357
Db CCACTTGAGCTCAGACCTCTAAACCCGTATTTCCCTTATGATGTCCTTTTTCGAGACA 3365
QY CTAAATTTTAAATACTTACTAGCTCTGAATATATATGATTTTATACAGATTTCTCAGG 3417
Db CTAAATTTTAAATACTTACTAGCTCTGAATATATATGATTTTATACAGATTTCTCAGG 3425
QY GTGAAATTAAACCAACTATAGGCTTTTCTTTGGGATGATTTTCTAGTCTTAAGTGTGG 3477
Db GTGAAATTAAACCAACTATAGGCTTTTCTTTGGGATGATTTTCTAGTCTTAAGTGTGG 3485
QY GGACATTATAAATCTGAGTACATTTGTTGTACACAGTTGATATTCCTTATGATGTCCTTTTTCGAGATG 3537
Db GGACATTATAAATCTGAGTACATTTGTTGTACACAGTTGATATTCCTTATGATGTCCTTTTTCGAGATG 3545
QY GGAGGAGAGGTGCTTAAAGCTGTAGGCTTTTCTTTGGGATGATTTTCTAGTCTTAAGTGTGG 3597
Db GGAGGAGAGGTGCTTAAAGCTGTAGGCTTTTCTTTGGGATGATTTTCTAGTCTTAAGTGTGG 3605
QY TTTAATATTTTTTAGAGATGTAACACATTTCTGCTTTCTTTAGTCTTAAGTGTGG 3657
Db TTTAATATTTTTTAGAGATGTAACACATTTCTGCTTTCTTTAGTCTTAAGTGTGG 3665
QY TTTTATTCAATAAGATTTTAAATTAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAA 3703
Db TTTTATTCAATAAGATTTTAAATTAATTTGAAAAATTTGAAAAATTTGAAAAATTTGAAAA 3711

RESULT 4
AAZ33566
ID AAZ33566 standard; cDNA; 2783 BP.
XX
AC AAZ33566;
XX
DT 08-DEC-1999 (first entry)
XX
DE Human breast tumour-associated EST 26.
XX
KW Expressed sequence tag; EST; human; breast; cancer; cytostatic;
KW medicaments; gene therapy; treatment; fat metabolism; ss.
XX
OS Homo sapiens.
XX
PN DE19813835-A1.
XX
PD 23-SEP-1999.
XX
PF 20-MAR-1998; 98DE-1013835.
XX
PR 20-MAR-1998; 98DE-1013835.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
XX
DR WPI; 1999-528979/45.
XX
DR P-PSDB; AAY48487.
XX
PT Human nucleic acid sequences and protein products from normal breast
XX tissue, useful for breast cancer therapy

PS Claim 1a; 113-114; 206pp; German.
XX This invention describes novel human nucleic acid sequences from normal breast tissue which have cytostatic activity. The nucleic acid sequences can be used to produce and isolate full-length gene sequences. They can be used to express proteins, which can be used as tools to find an activity against breast cancer. The sequences can be used in sense or antisense form. They are especially useful for medicaments for gene therapy to treat breast cancer and for treating illnesses associated with fat metabolism. AAZ33541-Z33610 represent expressed sequence tags described in the method of the invention.
SQ Sequence 2783 BP; 901 A; 527 C; 608 G; 747 T; 0 other;
Query Match 70.18; Score 2596; DB 20; Length 2783;
Best Local Similarity 99.98; Pred. No. 0;
Matches 2696; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1001 AATGAGCTGAAAGCCAGTGTGGGAAATCAAAATTCATAAAATGGAGCAAAAGGAGAAT 1060
Db 40 AATGAGCTGAAAGCCAGTGTGGGAAATCAAAATTCATAAAATGGAGCAAAAGGAGAAT 99
QY 1061 GTGCCCCCAGGTCTCTGAGTCTGCATCAACCATCAGGAAGGGGAAAGATTTCTGCAAAAT 1120
Db 100 GTGCCCCCAGGTCTCTGAGTCTGCATCAACCATCAGGAAGGGGAAAGATTTCTGCAAAAT 159
QY 1121 GAGAATAGCTGCGAGTCCGTTCCACCCCTGCCGAAGATGACTCCCGTGAATCCCAGGTT 1180
Db 160 GAGAATAGCTGCGAGTCCGTTCCACCCCTGCCGAAGATGACTCCCGTGAATCCCAGGTT 219
QY 1181 AAGAGTGAAGTTCACAGAGCTGTCCATCCAGCCACTAAGTCCAGATTCAGAGGCTCC 1240
Db 220 AAGAGTGAAGTTCACAGAGCTGTCCATCCAGCCACTAAGTCCAGATTCAGAGGCTCC 279
QY 1241 AGTCTTTCTGAAAGTCTCTCTCCAAAGCAATGAAGAGTTTCAGGCACCTGCAAGAGAG 1300
Db 280 AGTCTTTCTGAAAGTCTCTCTCCAAAGCAATGAAGAGTTTCAGGCACCTGCAAGAGAG 339
QY 1301 ACCTGCTGGAATGTCAGAAAGCAGTCTATCCAATGGAGCGTCTCTTGGCCCAACAGCAG 1360
Db 340 ACCTGCTGGAATGTCAGAAAGCAGTCTATCCAATGGAGCGTCTCTTGGCCCAACAGCAG 399
QY 1361 GTGTTTTCACATCAGTCTTCCGTTGCTCTATTCGAACAACAACTAGTCTAGGAACA 1420
Db 400 GTGTTTTCACATCAGTCTTCCGTTGCTCTATTCGAACAACAACTAGTCTAGGAACA 459
QY 1421 TATGCATCTTTACATGGAAGATCTATTGTAAGCTCACTTCAATCAACTTTTAAATCT 1480
Db 460 TATGCATCTTTACATGGAAGATCTATTGTAAGCTCACTTCAATCAACTTTTAAATCT 519
QY 1481 AAGGGCACTATGATGAAGGCTTTGGGCACAGACACCAAGGATCTATGGCAAGCAAA 1540
Db 520 AAGGGCACTATGATGAAGGCTTTGGGCACAGACACCAAGGATCTATGGCAAGCAAA 579
QY 1541 AATGAAAACGAGAGATTTTGGAGAGACCGCCAGCTTGCAAAATGCAAGGAGACCCCT 1600
Db 580 AATGAAAACGAGAGATTTTGGAGAGACCGCCAGCTTGCAAAATGCAAGGAGACCCCT 639
QY 1601 CACAGCCAGGGGTAGAAGATGCCCCCTATTGCTAAGGTGGGTGCTTGGCTGCAAGTATG 1660
Db 640 CACAGCCAGGGGTAGAAGATGCCCCCTATTGCTAAGGTGGGTGCTTGGCTGCAAGTATG 699
QY 1661 GAAGCCAAAGGCTCTCTCAGCAGGAGAAAGAACAGACAGCTGAAACCAAGAGCTG 1720
Db 700 GAAGCCAAAGGCTCTCTCAGCAGGAGAAAGAACAGACAGCTGAAACCAAGAGCTG 759
QY 1721 AGGATCCCTGGCCACCCCTCACTGAATCTTGAAGTTCAGGAAGTGCCTTGGAGAGAGG 1780
Db 760 AGGATCCCTGGCCACCCCTCACTGAATCTTGAAGTTCAGGAAGTGCCTTGGAGAGAGG 819
QY 1781 ATCAAAATGTCAAAGCCCAATGCTTGAAGACCAAAATCAGCAAGCCGAGTTCCT 1840
Db 820 ATCAAAATGTCAAAGCCCAATGCTTGAAGACCAAAATCAGCAAGCCGAGTTCCT 879

1841 GAGGATGTCGATCTAGATCTGAAGAAGCTAAGACGATCTTCTCACTGAAGGAAAGAC 1900
Db |||||
880 GAGGATGTCGATCTAGATCTGAAGAAGCTAAGACGATCTTCTCACTGAAGGAAAGAC 939
QY |||||
1901 CGCCCATTCACCTGACGCTTCAATTTCAAGACACCTCTGTCAGAGGCCCAAAACTGTG 1960
Db |||||
940 CGCCCATTCACCTGACGCTTCAATTTCAAGACACCTCTGTCAGAGGCCCAAAACTGTG 999
QY |||||
1961 TCCCAACCTATCAGGAAAGGCTGGAGCATGTCTAGAGCAGAGTGAAGAGTCTGTGGGTGA 2020
Db |||||
1000 TCCCAACCTATCAGGAAAGGCTGGAGCATGTCTAGAGCAGAGTGAAGAGTCTGTGGGTGA 1059
QY |||||
2021 AGAGTTGCGAAGAAAGAACTGGAATAATGCCAAGGCTTCTAAGAAATGGGAATGTG 2080
Db |||||
1060 AGAGTTGCGAAGAAAGAACTGGAATAATGCCAAGGCTTCTAAGAAATGGGAATGTG 1119
QY |||||
2081 GGAATAAACACCTGCGAATAACAAAGTCTAAGAGGAGAGACAGGGAAGAGTAAGGAA 2140
Db |||||
1120 GGAATAAACACCTGCGAATAACAAAGTCTAAGAGGAGAGACAGGGAAGAGTAAGGAA 1179
QY |||||
2141 GGTATAGTTGGAGATGGAGATGAGAAATCTTGTAGAAATGGTGCAGACTCCGATGAA 2200
Db |||||
1180 GGTATAGTTGGAGATGGAGATGAGAAATCTTGTAGAAATGGTGCAGACTCCGATGAA 1239
QY |||||
2201 GATGATAACAGCTTCTTCAAAACAACTCTCCACAGAAACCAAGTCTCTGAAATGGTGC 2260
Db |||||
1240 GATGATAACAGCTTCTTCAAAACAACTCTCCACAGAAACCAAGTCTCTGAAATGGTGC 1299
QY |||||
2261 AGTTTGTAGACAAACCTTCTGTAAGAAATCTCACTACTCAGATTCAGAAATCCAGGAT 2320
Db |||||
1300 AGTTTGTAGACAAACCTTCTGTAAGAAATCTCACTACTCAGATTCAGAAATCCAGGAT 1359
QY |||||
2321 GTGGAATCTCTGGAGGAGAGTGTCTCAAGAGCTCTCTGGAAGAAACCAAGTCTCTG 2380
Db |||||
1360 GTGGAATCTCTGGAGGAGAGTGTCTCAAGAGCTCTCTGGAAGAAACCAAGTCTCTG 2419
QY |||||
2381 AATCGGTATTAATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 2440
Db |||||
1420 AATCGGTATTAATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 1479
QY |||||
2441 AAATTCATGTTAGTGTAGGAGGACCTGCGCTTTGTCAAAATGTGTATGACATTAAGCAG 2500
Db |||||
1480 AAATTCATGTTAGTGTAGGAGGACCTGCGCTTTGTCAAAATGTGTATGACATTAAGCAG 1539
QY |||||
2501 GTATCCAGCATGAAATGTAATTTACTTGGAGTAACTTTTGGAAAGAAATTCCTTCTTAA 2560
Db |||||
1540 GTATCCAGCATGAAATGTAATTTACTTGGAGTAACTTTTGGAAAGAAATTCCTTCTTAA 1599
QY |||||
2561 AATCAAAAAACAAAAACAAAAACAAAAACAACTTCTAAATAGTACGATTAACCTTTAC 2620
Db |||||
1600 AATCAAAAAACAAAAACAAAAACAAAAACAACTTCTAAATAGTACGATTAACCTTTAC 1659
QY |||||
2621 TTAATTTCTTCAATTTAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 2680
Db |||||
1660 TTAATTTCTTCAATTTAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1719
QY |||||
2681 AAATATCCACCTGATAATAGCCAGATCTACTGTATTTCCCAAAAGGCAATATTAAAGT 2740
Db |||||
1720 AAATATCCACCTGATAATAGCCAGATCTACTGTATTTCCCAAAAGGCAATATTAAAGT 1779
QY |||||
2741 AGATAGATGATTAGTATGATATGTTACACACTATTTTGGAAATAGAGAACATACAGAG 2800
Db |||||
1780 AGATAGATGATTAGTATGATATGTTACACACTATTTTGGAAATAGAGAACATACAGAG 1839
QY |||||
2801 GAATTTAGGGCTTAAACATACGATGAATGACCTTTAGTATAAGGCGACAGTTTGA 2860
Db |||||
1840 GAATTTAGGGCTTAAACATACGATGAATGACCTTTAGTATAAGGCGACAGTTTGA 1899
QY |||||
2861 TATTTTAAATGAATACCAATTAATTTTATGATTTTACCTGTTAAGAGATTTATTTAGT 2920
Db |||||
1900 TATTTTAAATGAATACCAATTAATTTTATGATTTTACCTGTTAAGAGATTTATTTAGT 1959

2921 CTTTAAATTTTCTAGGTTAAATTTTCTGCTGTGATATATATGAGGAATTTTACTACTTTAT 2980
Db |||||
1960 CTTTAAATTTTCTAGGTTAAATTTTCTGCTGTGATATATATGAGGAATTTTACTACTTTAT 2019
QY |||||
2981 GTCTGCTCTCTAAACTACATCTGAACTCGACCTCTGAGGTATATATACAAACAGAGCAC 3040
Db |||||
2020 GTCTGCTCTCTAAACTACATCTGAACTCGACCTCTGAGGTATATATACAAACAGAGCAC 2079
QY |||||
3041 TTTTGTAGGCAATTTGAAAAACCAACCTACACTCTTCCGTGCTTAGAGAGATCTGCTGCT 3100
Db |||||
2080 TTTTGTAGGCAATTTGAAAAACCAACCTACACTCTTCCGTGCTTAGAGAGATCTGCTGCT 2139
QY |||||
3101 CCCAAATTAAGCTTTTGTATCTGCCAGTGAATTTACTGTACTCCAAATGATTTGCTTTCT 3160
Db |||||
2140 CCCAAATTAAGCTTTTGTATCTGCCAGTGAATTTACTGTACTCCAAATGATTTGCTTTCT 2199
QY |||||
3161 TCTGGTCATATCTGTGCTCTCATATTTACTGAAAGCTGCAATATTTTAGTAATACCTTC 3220
Db |||||
2200 TCTGGTCATATCTGTGCTCTCATATTTACTGAAAGCTGCAATATTTTAGTAATACCTTC 2259
QY |||||
3221 GGGATCACTCTCCCACTCTTCCGTGTTAGAGCAAAAGTGAAGAGTTTAAAGGAGGAAGAA 3280
Db |||||
2260 GGGATCACTCTCCCACTCTTCCGTGTTAGAGCAAAAGTGAAGAGTTTAAAGGAGGAAGAA 2319
QY |||||
3281 GAAAGAACTGTCTTACACCACTTTGAGCTCAGACCTCTAAACCCCTGTATTTCCCTTATGAT 3340
Db |||||
2320 GAAAGAACTGTCTTACACCACTTTGAGCTCAGACCTCTAAACCCCTGTATTTCCCTTATGAT 2379
QY |||||
3341 GTCCCTCTTTTGAGACACTAAATTTTAAATACTTACTAGCTCTGAAATATATTTGATTTTT 3400
Db |||||
2380 GTCCCTCTTTTGAGACACTAAATTTTAAATACTTACTAGCTCTGAAATATATTTGATTTTT 2439
QY |||||
3401 ATCAGATATTTCTCAGGTTGAAATTAACCACTATAGGCTTTTCTTGGGATGATTTT 3460
Db |||||
2440 ATCAGATATTTCTCAGGTTGAAATTAACCACTATAGGCTTTTCTTGGGATGATTTT 2499
QY |||||
3461 CTAGCTTAAAGTTTGGGACACTTAAACTTGAAGTACATTTTGTGTACACAGTTGATAT 3520
Db |||||
2500 CTAGCTTAAAGTTTGGGACACTTAAACTTGAAGTACATTTTGTGTACACAGTTGATAT 2559
QY |||||
3521 TCCAAATTTGTATGGATGGAGGAGAGGTGCTTAAAGCTGTAGGCTTTTCTTTGACTGC 3580
Db |||||
2560 TCCAAATTTGTATGGATGGAGGAGAGGTGCTTAAAGCTGTAGGCTTTTCTTTGACTGC 2619
QY |||||
3581 ATTATAGAGATTTAGCTTTTAAATTTTGTAGAGATGTAACCATTTCTGCTTTCTTAGTC 3640
Db |||||
2620 ATTATAGAGATTTAGCTTTTAAATTTTGTAGAGATGTAACCATTTCTGCTTTCTTAGTC 2679
QY |||||
3641 TTACCTAGTCTCAACATTTTATTAATTAAGATTTTAAATTAAGATTTTAAATTTGAAAAAAA 3698
Db |||||
2680 TTACCTAGTCTCAACATTTTATTAATTAAGATTTTAAATTTGAAAAAAA 2737

RESULT 5

ABK35261

ID ABK35261 standard; cDNA; 2749 BP.

XX AC ABK35261;

XX DT 08-MAY-2002 (first entry)

XX DE Human cDNA encoding secreted protein #399.

XX KW Human; secreted protein; gene; ss; nutritional supplement; haemophilia;

XX KW viral infection; bacterial infection; fungal infection; diabetes; asthma;

XX KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumor;

XX KW Alzheimer's disease; Parkinson's disease; neurodegenerative disease;

XX KW coagulation disorder; inflammatory disorder; Crohn's disease; ulcer;

XX KW tissue regeneration; wound healing; burn; haematopoiesis;

XX KW myeloid cell deficiency; lymphoid cell deficiency.

XX OS Homo sapiens.

XX PN WO200177288-A2.
XX PD 18-OCT-2001.
XX PF 29-MAR-2001; 2001WO-US10224.
XX PR 06-APR-2000; 2000US-195582P.
XX PA (GEMY) GENETICS INST INC.
XX
PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
PI Gulukota K, Graham JR;
XX WPI; 2002-179321/23.
XX
PT Five hundred and ninety two polynucleotides derived from a variety of
PT human tissue sources which encode secreted proteins, useful for
PT treating immune deficiencies and disorders such as autoimmune disorders
PT -
XX
PS Claim 1; Page 279-280; 372pp; English.
XX
CC The invention relates to 592 polynucleotides which have been derived from
CC a variety of human tissue sources and which encode novel secreted
CC proteins. The polynucleotides can be used as probes for the
CC identification and isolation of full length cDNA and genomic DNA. The
CC polynucleotides and proteins can also be used as nutritional supplements.
CC The proteins are useful in the treatment of various immune deficiencies
CC and disorders such as viral infections, bacterial infections, fungal
CC infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple
CC sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions
CC and conditions (e.g. asthma). They are also useful for treating
CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
CC disease), liver fibrosis, coagulation disorders (e.g. haemophilia),
CC inflammatory disorders (e.g. Crohn's disease) and tumours. They are also
CC useful for tissue regeneration, for wound healing and in the treatment of
CC burns, incisions and ulcers. The proteins are also useful for regulating
CC haematopoiesis and for treating myeloid or lymphoid cell deficiencies.
CC Sequences ABK34863-ABK35454 represent polynucleotides of the invention.
XX
SQ Sequence 2749 BP; 885 A; 535 C; 593 G; 736 T; 0 other;

Query Match 69.9%; Score 2589; DB 24; Length 2749;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2639; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1051 AAAGGAGATGTGCCCCAGGTCCTGAGTGTGTCATCCCATCAGGAAGGGGAAAGAT 1110
DB 110 AAAGGAGATGTGCCCCAGGTCCTGAGTGTGTCATCCCATCAGGAAGGGGAAAGAT 169

QY 1111 TTCTGCAATGAGATAGCCTGGCAGTCCGTTCCACCCCTGCCGAAGATGACTCCCGTGA 1170
DB 170 TTCTGCAATGAGATAGCCTGGCAGTCCGTTCCACCCCTGCCGAAGATGACTCCCGTGA 229

QY 1171 CTCCGAGTTAAGAGTGAAGTTCAACAGCTGTCCATCCCAAGCCACTAAGTCAGATTTC 1230
DB 230 CTCCGAGTTAAGAGTGAAGTTCAACAGCTGTCCATCCCAAGCCACTAAGTCAGATTTC 289

QY 1231 CAGAGCTTCCAGTCTTCTGTAAGTCTCTCCCTCCCAAGCAATGAAGATTTCAGGCACC 1290
DB 290 CAGAGCTTCCAGTCTTCTGTAAGTCTCTCCCTCCCAAGCAATGAAGATTTCAGGCACC 349

QY 1291 TGCAGAGAGACCTGCGTGGAAATGTCAGAGACAGTCTATCCATGGAGGCTCTCTTGGC 1350
DB 350 TGCAGAGAGACCTGCGTGGAAATGTCAGAGACAGTCTATCCATGGAGGCTCTCTTGGC 409

QY 1351 CAACCCAGAGTGTTCACATCAGCTGCTTCCGTTGCTCTCTATTGCAACAACAACCTCAG 1410
DB 410 CAACCCAGAGTGTTCACATCAGCTGCTTCCGTTGCTCTCTATTGCAACAACAACCTCAG 469

QY 1411 TCTAGGAACATATGCATCTTACATGGAAGATCTATTGTAAGCTCCTCAATCAACT 1470
DB 1470 TCTAGGAACATATGCATCTTACATGGAAGATCTATTGTAAGCTCCTCAATCAACT 1609

DB 470 TCTAGGAACATATGCATCTTACATGGAAGATCTATTGTAAGCTCCTCAATCAACT 529
QY 1471 CTTTAAATCTAAGGGCAACTATGATGAAGGCTTTGGGCACAGACACACAGGATCTATG 1530
DB 530 CTTTAAATCTAAGGGCAACTATGATGAAGGCTTTGGGCACAGACACACAGGATCTATG 589
QY 1531 GCACAGCAAAATGAAACGAAAGAGATTTTGGAGAGACAGCCAGCTTGCAAAATGCAAG 1590
DB 590 GCACAGCAAAATGAAACGAAAGAGATTTTGGAGAGACAGCCAGCTTGCAAAATGCAAG 649
QY 1591 GGAGACCCCTCACAGCCAGGGGTAGAAGATGCCCCCTATTGCTAAGGTGGTCTCTGGC 1650
DB 650 GGAGACCCCTCACAGCCAGGGGTAGAAGATGCCCCCTATTGCTAAGGTGGTCTCTGGC 709
QY 1651 TGCAAGTATGGAAGCCAGGCTCTCTCTCAGCAGAGAGAAAGCAAGCAGCTGAAAC 1710
DB 710 TGCAAGTATGGAAGCCAGGCTCTCTCTCAGCAGAGAGAAAGCAAGCAGCTGAAAC 769
QY 1711 CAAGAAGCTGAGGATGCGCTGGCCACCCCTGAACTTGAAGTTTGAAGAGTGCCTT 1770
DB 770 CAAGAAGCTGAGGATGCGCTGGCCACCCCTGAACTTGAAGAGTGCCTT 829
QY 1771 GGAGAGGGATCAAAATGTCAAAGCCCAATGSCCTCTGAAAGCAAAATCAACAAGCC 1830
DB 830 GGAGAGGGATCAAAATGTCAAAGCCCAATGSCCTCTGAAAGCAAAATCAACAAGCC 889
QY 1831 CGAAGTCTCTGAGATGTGATCTAGATCTGAAGAACTAAGACGATCTTCTTCACTGAA 1890
DB 890 CGAAGTCTCTGAGATGTGATCTAGATCTGAAGAACTAAGACGATCTTCTTCACTGAA 949
QY 1891 GGAAGAAGCGCCCATCTACTGTAGCAGCTTCATTTCAAAGCACCTCTGTCAAGAGCCC 1950
DB 950 GGAAGAAGCGCCCATCTACTGTAGCAGCTTCATTTCAAAGCACCTCTGTCAAGAGCCC 1009
QY 1951 AAAAATCTGTCTCCCACTATCAGGAAAGGCTGGAGCATGTCAAGCAGAGTGAAGAGTC 2010
DB 1010 AAAAATCTGTCTCCCACTATCAGGAAAGGCTGGAGCATGTCAAGCAGAGTGAAGAGTC 1069
QY 2011 TGTGGTGAAGAGTGTCCAGAAAGGAAACAAAGTGGAAATGCCAAAGCTTCTTAAGAAGAA 2070
DB 1070 TGTGGTGAAGAGTGTCCAGAAAGGAAACAAAGTGGAAATGCCAAAGCTTCTTAAGAAGAA 1129
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DB 1130 TGGGAATGTGGGAAACAAACCTGGGCAAAACAAAGAAATCTAAAGGAGAGACGGGAAGAG 1189
QY 2131 AAGTAAGGAAAGTCTAGTGTGGAGATGGAGATGAGATCTTGTAGAAAATGGTGACA 2190
DB 1190 AAGTAAGGAAAGTCTAGTGTGGAGATGGAGATGAGATCTTGTAGAAAATGGTGACA 1249
QY 2191 CTCGATGAAGATGATAACAGCTTCTCTCAAAACAACTCTCCACAGAAACCCCAAGTCTCT 2250
DB 1250 CTCGATGAAGATGATAACAGCTTCTCTCAAAACAACTCTCCACAGAAACCCCAAGTCTCT 1309
QY 2251 GAATTCGTGAGTTTGTAGACAAACCTTTCTCTGAAGAAATTCCTACTCAGAAATCAGAA 2310
DB 1310 GAATTCGTGAGTTTGTAGACAAACCTTTCTCTGAAGAAATTCCTACTCAGAAATCAGAA 1369
QY 2311 ATCCCAGGATGTGGACTCTGGGAGGGAAGTGGTCAAGAGCTCTCTGTGGAGAGAA 2370
DB 1370 ATCCCAGGATGTGGACTCTGGGAGGGAAGTGGTCAAGAGCTCTCTGTGGAGAGAA 1429
QY 2371 GATAAGAGAAATCGGTATTATGATGAGGATGAGGATGAAGAGTGCACAAATTCGATGAT 2430
DB 1430 GATAAGAGAAATCGGTATTATGATGAGGATGAGGATGAAGAGTGCACAAATTCGATGAT 1489
QY 2431 GCTGGGCTTAAATTCATGTTAGTGTAGCGAGCCACTGCCCTTTGTCAAAATGTGATGC 2490
DB 1490 GCTGGGCTTAAATTCATGTTAGTGTAGCGAGCCACTGCCCTTTGTCAAAATGTGATGC 1549
QY 2491 ACATAGCAGGTATCCAGCATGAATGTAATTTACTTGGAGTAACTTTGGAAGAAAT 2550
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Best Local Similarity 100.0%; Pred. No. 0; Matches 2565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	22	TAGCAGCTTGGTCGCGACAGGTGCGCTAGGTAGAGCGCCGGGACCTGTGACAGGGCTGCT	81
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QY	82	AGCAGCGCAGAGAAAGGGGGCTTTTAGCCAGGTATTTTCAGTGTCTGTAGACAAGATGGA	141
Db	118	AGCAGCGCAGAGAAAGGGGGCTTTTAGCCAGGTATTTTCAGTGTCTGTAGACAAGATGGA	177
QY	142	ATCATCTCATTTAATAGACGGCAATGGACCTCACTATCATTTGAGGGTAACAGCCAAAGA	201
Db	178	ATCATCTCATTTAATAGACGGCAATGGACCTCACTATCATTTGAGGGTAACAGCCAAAGA	237
QY	202	ACTTTCTCTTGTCAACAAAGCAAGTCATCGGCTATTGTGGAAATATTCTTCCAAATACCA	261
Db	238	ACTTTCTCTTGTCAACAAAGCAAGTCATCGGCTATTGTGGAAATATTCTTCCAAATACCA	297
QY	262	GAAGCAGCTGAAGAAACAAACATGGAGAAAGAGAGTAACACCGGAAATCTCTCCCA	321
Db	298	GAAGCAGCTGAAGAAACAAACATGGAGAAAGAGAGTAACACCGGAAATCTCTCCCA	357
QY	322	GCACCTTTAGAAAGGGGACCCCTCACTGTGTGTTAAAGAAAGAGTGGGAGAACCCAGGGCTGG	381
Db	358	GCACCTTTAGAAAGGGGACCCCTCACTGTGTGTTAAAGAAAGAGTGGGAGAACCCAGGGCTGG	417
QY	382	AGCAGAGTCTCACAGAGACTCTCTAGGNAAGCAGCAGCTGAGATTAGGCACAGACAGA	441
Db	418	AGCAGAGTCTCACAGAGACTCTCTAGGNAAGCAGCAGCTGAGATTAGGCACAGACAGA	477
QY	442	CCATCTCTCTGCTGAAGTGACAAAGCCACGCTGCTTCTGGAGCCCAAGCTGACCAAGAGA	501
Db	478	CCATCTCTCTGCTGAAGTGACAAAGCCACGCTGCTTCTGGAGCCCAAGCTGACCAAGAGA	537
QY	502	ACAAATCCACCCACAGATCTAGACTCAGGTCACCTCCTGAAGCCCTCGTTTCAGGGTCGATA	561
Db	538	ACAAATCCACCCACAGATCTAGACTCAGGTCACCTCCTGAAGCCCTCGTTTCAGGGTCGATA	597
QY	562	TCCCAATCAAGGACGCTGAGGATCTTTAAAGACCACTCAACAGAAAGTAAAAAAATGGA	621
Db	598	TCCCAATCAAGGACGCTGAGGATCTTTAAAGACCACTCAACAGAAAGTAAAAAAATGGA	657
QY	622	AAATTTGCTAGGAGAACTCAAGGCAATGAAGTAGAAGAAATCAGAAATCAGTGAAGACAGA	681
Db	658	AAATTTGCTAGGAGAACTCAAGGCAATGAAGTAGAAGAAATCAGAAATCAGTGAAGACAGA	717
QY	682	TGCTTCGGGCAAAATAGAGAAATATAATGTTCCGCTGAAACAGGCTTAAGATGATGTTGA	741
Db	718	TGCTTCGGGCAAAATAGAGAAATATAATGTTCCGCTGAAACAGGCTTAAGATGATGTTGA	777
QY	742	GAAAGGTGAACCAACTCAAACTAAGATTCTCCGGGCCCAAGCGGAAAGTCAAGTGGAG	801
Db	778	GAAAGGTGAACCAACTCAAACTAAGATTCTCCGGGCCCAAGCGGAAAGTCAAGTGGAG	837
QY	802	GAAGATCTTGAAACAGCTATTCTCTAGATGACCTGGAAATAGGCCCCAGGTGAGTTGTC	861
Db	838	GAAGATCTTGAAACAGCTATTCTCTAGATGACCTGGAAATAGGCCCCAGGTGAGTTGTC	897
QY	862	ATCTTCTACATTTGACTCGGAGAAATAGAGTAGACGAAATCTGGAACTTCCAGCCT	921
Db	898	ATCTTCTACATTTGACTCGGAGAAATAGAGTAGACGAAATCTGGAACTTCCAGCCT	957
QY	922	CTCAGAAACCTCTATAAGGATCGAATGGCCAAAGTACCAGGAGCTGTGTGCCAAACAAAG	981
Db	958	CTCAGAAACCTCTATAAGGATCGAATGGCCAAAGTACCAGGAGCTGTGTGCCAAACAAAG	1017
QY	982	CAGCTCAACCACTATACAAATCAGCTGAAGCAGGTGCTGGCGAAATCAAAATTCATAA	1041
Db	1018	CAGCTCAACCACTATACAAATCAGCTGAAGCAGGTGCTGGCGAAATCAAAATTCATAA	1077
QY	1042	AATGGAGCAAAAGGAGAAATGTGCCCCAGGTCTCTGAGGTCTCCATCACCCTATCAGGAAG	1101
Db			

Db	1078	AATGAGCAAAAGAGGAATGTGCCCCAGGTCCTGAGGTCTGCATCACCCTACGGAAGG	1137
QY	1102	GGAAGAATTTCTCAAAATGAGAATAGCCTGGCAGTCCGTTCCACCCCTCCCGAGATGA	1161
Db	1138	GGAAGAATTTCTCAAAATGAGAATAGCCTGGCAGTCCGTTCCACCCCTCCCGAGATGA	1197
QY	1162	CTCCCGTACTCCCAAGTTAAGAGTGAGGTTCAACAGCCTGTCCATCCCAGCCACTAAG	1221
Db	1198	CTCCCGTACTCCCAAGTTAAGAGTGAGGTTCAACAGCCTGTCCATCCCAGCCACTAAG	1257
QY	1222	TCCAGATTCAGAGCCTCCAGTCTTTCTGAAAGTTCTCTCCCAAAAGCAATGAAGAAGTT	1281
Db	1258	TCCAGATTCAGAGCCTCCAGTCTTTCTGAAAGTTCTCTCCCAAAAGCAATGAAGAAGTT	1317
QY	1282	TCAGGCACCTGCAAGAGAGACCTGCGTGGAAATGTCAAGACAGTCTATCCAATGGAGCG	1341
Db	1318	TCAGGCACCTGCAAGAGAGACCTGCGTGGAAATGTCAAGACAGTCTATCCAATGGAGCG	1377
QY	1342	TCTCTTGGCCAAACAGCAGGCTTTTTCACATCAGCTGCTTCCGTTGCTCTATTGCAACAA	1401
Db	1378	TCTCTTGGCCAAACAGCAGGCTTTTTCACATCAGCTGCTTCCGTTGCTCTATTGCAACAA	1437
QY	1402	CAAACTCAGTCTAGGAACATATGCATCTTTTACATGGAAGAAATCTATTGTAAGCCTCACTT	1461
Db	1438	CAAACTCAGTCTAGGAACATATGCATCTTTTACATGGAAGAAATCTATTGTAAGCCTCACTT	1497
QY	1462	CAATCACTCTTTAAATCTTAAGGGCAACTATGATGAAGGCTTTGGGCACAGACACACAA	1521
Db	1498	CAATCACTCTTTAAATCTTAAGGGCAACTATGATGAAGGCTTTGGGCACAGACACACAA	1557
QY	1522	GGATCTATGGGCAAGCAAAATGAAACGAAGAGATTTTGGAGAGACCCAGCCTTGC	1581
Db	1558	GGATCTATGGGCAAGCAAAATGAAACGAAGAGATTTTGGAGAGACCCAGCCTTGC	1617
QY	1582	AAATGCAAGGAGACCCCTCACAGCCAGGGGTAGAAGATGCCCCCTATTGCTAAGGTGG	1641
Db	1618	AAATGCAAGGAGACCCCTCACAGCCAGGGGTAGAAGATGCCCCCTATTGCTAAGGTGG	1677
QY	1642	TGTCCTGGCTGCAAGTATGGAAGCCAAAGGCTCTCTCAGCAGGAGAAAGACAAAGCC	1701
Db	1678	TGTCCTGGCTGCAAGTATGGAAGCCAAAGGCTCTCTCAGCAGGAGAAAGACAAAGCC	1737
QY	1702	AGCTGAAAACAAAGAGCTCAGGATCGCCTGGCCACCCCTCACTGAACTTTGGAAGTTCAG	1761
Db	1738	AGCTGAAAACAAAGAGCTCAGGATCGCCTGGCCACCCCTCACTGAACTTTGGAAGTTCAG	1797
QY	1762	AAGTGCCTTTGGAGGAAGGATCAAAATGTCAAGCCCAAAATGCGCTCTCTGAAGACGAAT	1821
Db	1798	AAGTGCCTTTGGAGGAAGGATCAAAATGTCAAGCCCAAAATGCGCTCTCTGAAGACGAAT	1857
QY	1822	CAGCAAGCCCGAAGTTCTCTGAGGATGTCATCTAGATCTGAAGAAAGCTAAGACGATCTTC	1881
Db	1858	CAGCAAGCCCGAAGTTCTCTGAGGATGTCATCTAGATCTGAAGAAAGCTAAGACGATCTTC	1917
QY	1882	TTCACTGGAAGGAAGCAAGCCGCCATTCCTGTAGCAGCTTCATTTCAAAGCACCTCTGT	1941
Db	1918	TTCACTGGAAGGAAGCAAGCCGCCATTCCTGTAGCAGCTTCATTTCAAAGCACCTCTGT	1977
QY	1942	CAAGAGCCCAAAAGCTGTGTCCCACTTATCAGGAAGGCTGGAGCATGTGAGACAGAG	2001
Db	1978	CAAGAGCCCAAAAGCTGTGTCCCACTTATCAGGAAGGCTGGAGCATGTGAGACAGAG	2037
QY	2002	TGAAGAGTCTTGGGTGGAAGAGTTGAGAAAGCAAGTGGAAATGCCAAGGCTTC	2061
Db	2038	TGAAGAGTCTTGGGTGGAAGAGTTGAGAAAGCAAGTGGAAATGCCAAGGCTTC	2097
QY	2062	TAAGAGAAATGGGAATGTGGGAAAAAACAACCTGCAAAACAAAGAAATCTTAAGGAGAGAC	2121
Db	2098	TAAGAGAAATGGGAATGTGGGAAAAAACAACCTGCAAAACAAAGAAATCTTAAGGAGAGAC	2157
QY	2122	AGGAAGAGAGTAAGGAAGTCTACTTTGGAGATGGAGAAATGAGAAATCTTTAGAAAA	2181
Db	2158	AGGAAGAGAGTAAGGAAGTCTACTTTGGAGATGGAGAAATGAGAAATCTTTAGAAAA	2217

QY 2182 TGGTCAGACTCCGATGAAGATGATAACAGCTTCTCTCAAAACAAATCTCCACAGAAC 2241
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Db 2218 TGGTCAGACTCCGATGAAGATGATAACAGCTTCTCTCAAAACAAATCTCCACAGAAC 2277
| | | | |
QY 2242 CAAGTCTCTGAATTCGGTCGAGTTTGTAGACACACCTTTCCTGAAGAAATCACTACTCA 2301
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Db 2278 CAAGTCTCTGAATTCGGTCGAGTTTGTAGACACACCTTTCCTGAAGAAATCACTACTCA 2337
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QY 2302 GAATCAGAAATCCAGGATGTGGAACTCTGGGAGGAGAGTGGTCAAGAGCTCTCTGT 2361
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Db 2338 GAATCAGAAATCCAGGATGTGGAACTCTGGGAGGAGAGTGGTCAAGAGCTCTCTGT 2397
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QY 2362 GGAAGAACAGATTAAGAGAAATCGGTATTATGATGAGGATGAGGATGAAGAGTGCACAAAT 2421
| | | | |
Db 2398 GGAAGAACAGATTAAGAGAAATCGGTATTATGATGAGGATGAGGATGAAGAGTGCACAAAT 2457
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QY 2422 TGCATGATGCTGGCCCTTAAATTCATGTTAGTTAGTGTACCGAGCCACTGCCCTTTGTCAAA 2481
| | | | |
Db 2458 TGCATGATGCTGGCCCTTAAATTCATGTTAGTTAGTGTACCGAGCCACTGCCCTTTGTCAAA 2517
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QY 2482 ATGTGATGCATTAAGCAGGATCCAGCATGAATGTAAATTTACTTTGGAAGTAACCTTTG 2541
| | | | |
Db 2518 ATGTGATGCATTAAGCAGGATCCAGCATGAATGTAAATTTACTTTGGAAGTAACCTTTG 2577
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QY 2542 GAAAGAAATTCCTTCTTAAATTCAAAAACAAAAACAAAAACAAAAACACA 2586
| | | | |
Db 2578 GAAAGAAATTCCTTCTTAAATTCAAAAACAAAAACAAAAACAAAAACACA 2622
| | | | |

RESULT 7
AAF55697
ID AAF55697 standard; DNA, 3650 BP.
XX
AC AAF55697;
XX
DT 11-JUN-2001 (first entry)
XX
DE Human EPLIN (epithelial protein lost in neoplasm)-beta isoform DNA.
XX
KW Human; EPLIN; epithelial protein lost in neoplasm; EPLIN-alpha;
KW EPLIN-beta; tumour suppressor; tumour; cell proliferative disorder;
KW gene therapy; cancer; ss.
XX
OS Homo sapiens.

Key Location/Qualifiers
CDS 102..2384
FT /*tag= a
FT /transl_except= "{pos: 933..935, aa: Val}"
FT /transl_except= "{pos: 1131..1136, aa: Arg}"
FT /transl_except= "{pos: 1587..1589, aa: Asp}"
FT /transl_except= "{pos: 1635..1637, aa: Lys}"
FT /transl_except= "{pos: 2068..2070, aa: Ser}"
FT /transl_except= "{pos: 2076..2078, aa: Ser}"
FT /transl_except= "{pos: 2139..2141, aa: Ile}"
FT /transl_except= "{pos: 2196..2198, aa: Ser}"
FT /transl_except= "{pos: 2214..2216, aa: Ser}"
FT /product= "EPLIN (epithelial protein lost in neoplasm)"
XX
PN WO200119019-A1.
XX
PD 15-MAR-2001.
XX
PD 08-SEP-2000; 2000WO-US24689.
XX
PR 08-SEP-1999; 99US-0153024.
XX (REGC) UNIV CALIFORNIA.
XX
PI Chang DD, Maul RS;
XX
DR WPI; 2001-244555/25.

DR P-PSDB; AAB67701.
XX
PT New tumor suppressor protein EPLIN, useful as a marker for diagnostic,
prognostic and therapeutic applications over the course of cell
proliferative disorders associated with EPLIN .
XX
PS Claim 4; Page 43-44; 59pp; English.
XX
CC The present sequence encodes a human EPLIN (epithelial protein lost in
neoplasm)-beta isoform. The specification also describes EPLIN-alpha.
CC EPLIN is a tumour suppressor protein, whose expression is altered in
CC multiple common human tumour types. EPLIN nucleic acids and proteins are
CC used in screening assays to detect molecules that specifically bind to
CC EPLIN nucleic acids, proteins or derivatives and thus have potential use
CC as agonist or antagonist of EPLIN, in particular molecules that affect
CC cell proliferation. Thus the assays are useful for screening molecules
CC with potential utility as anticancer drugs or lead compounds for drug
CC development. EPLIN nucleic acids, proteins are useful for detecting a
CC cell proliferative disorder in a subject. EPLIN polynucleotides are
CC useful in gene therapy techniques. EPLIN is useful as a marker that
CC can be diagnostically, prognostically and therapeutically used over
CC the course of a cell proliferative disorder associated with EPLIN.
XX
SQ Sequence 3650 BP; 1197 A; 733 C; 809 G; 911 T; 0 other;

Query Match 57.5%; Score 2130; DB 22; Length 3650;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3580; Conservative 0; Mismatches 11; Indels 11; Gaps 4;

QY 92 AGGAAAGCGGCTTTTAGCCAGGTATTTTCAGTGTCTGTAGACAAGATGGAATCATCTCCA 151
Db 57 AGGAAAGCGGCTTTTAGCCAGGTATTTTCAGTGTCTGTAGACAAGATGGAATCATCTCCA 116
| | | | |
QY 152 TTTAATAGACGCAATGACCTCCTATCATTTAGGGTAAACAGCCAAAGAACTTTCTCT 211
Db 117 TTTAATAGACGCAATGACCTCCTATCATTTAGGGTAAACAGCCAAAGAACTTTCTCT 176
| | | | |
QY 212 GTCAACAAGAACAGTCACTCGCTATTTGTGGAATATTTCTCAAGTACAGAAAGCAGCT 271
LJ 177 GTCAACAAGAACAGTCACTCGCTATTTGTGGAATATTTCTCAAGTACAGAAAGCAGCT 236
| | | | |
QY 272 GAAGAAACAAACATGGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 331
Db 237 GAAGAAACAAACATGGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 296
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QY 332 AAGGGACCTTGACTGTGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 391
Db 297 AAGGGACCTTGACTGTGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 356
| | | | |
QY 392 CACACAGACTCTCTACGGAACAGCAGCACTGAGATTAGGCACAGAGCAGACCATCTCTCT 451
Db 357 CACACAGACTCTCTACGGAACAGCAGCACTGAGATTAGGCACAGAGCAGACCATCTCTCT 416
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QY 452 GCTGAAGTGACAAGCCACGCTGCTTCTGGAGCCAAAGCTACCAAGAGAACAAATCCAC 511
Db 417 GCTGAAGTGACAAGCCACGCTGCTTCTGGAGCCAAAGCTACCAAGAGAACAAATCCAC 476
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Db 477 CCCAGATCTTAGACTCAGGTCACTCTGGAAGCCCTCGTTCCAGGGTCGATATCCCCACATC 536
| | | | |
QY 572 AAGGACGGTGAGGATCTTAAAGACCACTCAACAGAAAGTAAAAAATGGAAAAATTTGCTA 631
Db 537 AAGGACGGTGAGGATCTTAAAGACCACTCAACAGAAAGTAAAAAATGGAAAAATTTGCTA 596
| | | | |
QY 632 GGAGAAATCCAGGCATGAAGTAGAAAAATCAGAAATCAGTGAAGAACACAGATGCTCGGGC 691
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QY 692 AAAATAGAGAAATATATATGTTCCGCTGGAACAGCTTAAGATGATGTTTGAGAAAGTGAA 751
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QY 1736 CCCCCCACTGAACTTGGAAAGTTTCAAGAGTTCAGGAAGGATCAAAATGTCAAAAG 1795
Db 272 CCCCCCACTGAACTTGGAAAGTTTCAAGAGTTCAGGAAGGATCAAAATGTCAAAAG 331
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Db 332 CCCAAATGGCCCTCTGAAGACGAAATCAGCAAGCCCGAAAGTTCCTGAGGATGTCATCTA 391
QY 1856 GATCTGAAGAAGCTAAGACGATCTTCTTCACTGAAGGAAAGAGCGCCCATTCATCTGTA 1915
Db 392 GATCTGAAGAAGCTAAGACGATCTTCTTCACTGAAGGAAAGAGCGCCCATTCATCTGTA 451
QY 1916 GCGAGTTTCAATTTCAAAGCACTCTGTCAAGAGCCCAAAATCTGTGTCCTCCCATCTACAGG 1975
Db 452 GCGAGTTTCAATTTCAAAGCACTCTGTCAAGAGCCCAAAATCTGTGTCCTCCCATCTACAGG 511
QY 1976 AAAGGCTGGAGATGTCAGACGAGTGAAGAGTCTGTGGTGGGAAGTTCAGAAAAGG 2035
Db 512 AAAGGCTGGAGATGTCAGACGAGTGAAGAGTCTGTGGTGGGAAGTTCAGAAAAGG 571
QY 2036 AAACAAGTGGAAAATGCCAAGCTTCTTAAGAAAGATGGAATGTGGGAAACCAACCTGG 2095
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Db 692 ATGGAGATGAGAAATCTTGTAGAAAATGGTGCAGACTCCGATGAAGATGATAACAGCTTC 751
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Db 812 ACCTTTGTGAAGAAATTCACACTCAGAAATCCCAAGATGTGGAACTCTGGGAG 871
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Db 872 GGAGAAGTGTCAAGAGCTCTCTGTGGAAGACAGATAAAGAGAAATCGGTATTATGAT 931
QY 2396 GAGGATGAGGATGAAGAGTGAATAATGCAATGATGCTGGCCCTTAAATTCATGTTAGTG 2455
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QY 2516 ATGTAATTTACTTGGAAAGTAACTTTGAAAAGAAATTCCTTTTAAATCAAAAACAAAC 2575
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Db 1172 TAGCAGTGATGATGATGATGAATGCTGTAAAGGCTTGAAGGAAATATCCACCTGA 1231
QY 2696 TAATAGCCAGATCTACTGTATTCCTCAAAAGCAATATTAAGGTAGATGATGATGAT 2755
Db 1232 TAATAGCCAGATCTACTGTATTCCTCAAAAGCAATATTAAGGTAGATGATGATGAT 1291
QY 2756 AGTATATTGTTACACACTATTTTGGAAATTTAGAGAACATACAGAAAGTATAGGGCTTA 2815
Db 1292 AGTATATTGTTACACACTATTTTGGAAATTTAGAGAACATACAGAAAGTATAGGGCTTA 1351
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QY 2816 AACATTACGACTGAATGACACTTTTAGTATAAAGGCGACAGTTTGTATATTTTAAATGAAT 2875
Db 1352 AACATTACGACTGAATGACACTTTTAGTATAAAGGCGACAGTTTGTATATTTTAAATGAAT 1411
QY 2876 ACCAAATTAATTTTAAATTTTACCTGTTAAAGAGATTTATTTAGTCTTTAAATTTTATAG 2935
Db 1412 ACCAAATTAATTTTAAATTTTACCTGTTAAAGAGATTTATTTAGTCTTTAAATTTTATAG 1471
QY 2936 GTTAATTTTCTGCTGTGATATATATAGGAAATTTACTACTTTATGTCTGCTCTCTAAA 2995
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QY 2996 CTACATCTGAACTGACGCTCTGAGGTATAATAACAACAGAGCACCTTTTGGAGCAATG 3055
Db 1532 CTACATCTGAACTGACGCTCTGAGGTATAATAACAACAGAGCACCTTTTGGAGCAATG 1591
QY 3056 AAAAAACCAACCTACACCTTTCCGCTTTAGAGAGATCTGCTGTCTCCCAAAATAGCTTTT 3115
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QY 3116 GTATCTGCCAGTGAATTTACTGTACTCCAAATGATTTTGTAGTAATACCTTCGGATCACTGCTCC 3175
Db 1652 GTATCTGCCAGTGAATTTACTGTACTCCAAATGATTTTGTAGTAATACCTTCGGATCACTGCTCC 1711
QY 3176 GCTTCTCATTAATTTACTGAAAGCTGCAATATTTTAGTAATACCTTCGGATCACTGCTCC 3235
Db 1712 GCTTCTCATTAATTTACTGAAAGCTGCAATATTTTAGTAATACCTTCGGATCACTGCTCC 1771
QY 3236 CATCTTCCGCTTTAGAGCAAAAGTGAAGAGTTTAAAGAGGAAAGAAAGAACTGCTCTTA 3295
Db 1772 CATCTTCCGCTTTAGAGCAAAAGTGAAGAGTTTAAAGAGGAAAGAAAGAACTGCTCTTA 1831
QY 3296 CACCACCTTGAGCTCAGACCTCTAAACCCCTGTATTTCCCTTATGATGTCCTCTTTTGGAG 3355
Db 1832 CACCACCTTGAGCTCAGACCTCTAAACCCCTGTATTTCCCTTATGATGTCCTCTTTTGGAG 1891
QY 3356 CACTAATTTTAAATACCTTACTAGCTCTGAAATATATTGATTTTATCACAGTATTCTCA 3415
Db 1892 CACTAATTTTAAATACCTTACTAGCTCTGAAATATATTGATTTTATCACAGTATTCTCA 1951
QY 3416 GGGTGAATTAACCAACTATAGGCTTTTCTGGGATGATTTTCTAGTCTTAAAGGTTT 3475
Db 1952 GGGTGAATTAACCAACTATAGGCTTTTCTGGGATGATTTTCTAGTCTTAAAGGTTT 2011
QY 3476 GGGACATTTATAAATCTTGAGTACATTTGTTGACACAGTTGATATCCAAATTTGATGGA 3535
Db 2012 GGGACATTTATAAATCTTGAGTACATTTGTTGACACAGTTGATATCCAAATTTGATGGA 2071
QY 3536 TGGGAGGAGAGGCTGCTTAAAGCTGTAGCTTTTCTTTGTTACTGCAATTTATAGAGTTTA 3595
Db 2072 TGGGAGGAGAGGCTGCTTAAAGCTGTAGCTTTTCTTTGTTACTGCAATTTATAGAGTTTA 2131
QY 3596 GCTTTAATTTTTPAGAGATGTAAACATTTCTGCTTTCTTTAGTCTTACCTAGTCTGAAA 3655
Db 2132 GCTTTAATTTTTPAGAGATGTAAACATTTCTGCTTTCTTTAGTCTTACCTAGTCTGAAA 2191
QY 3656 CATTTTATTTCAATAAGATTTTAAATTTTAAATTTT 3689
Db 2192 CATTTTATTTCAATAAGATTTTAAATTTTAAATTTT 2225
```

RESULT 9

AAF55696

ID AAF55696 standard; DNA; 3543 BP.

XX AAF55696;

AC AAF55696;

XX 11-JUN-2001 (first entry)

XX Human EPLIN (epithelial protein lost in neoplasm)-alpha isoform DNA.

DE Human; EPLIN; epithelial protein lost in neoplasm; EPLIN-alpha;

XX EPLIN-beta; tumour suppressor; tumour; cell proliferative disorder;

KW

KW gene therapy; cancer; ss.
XX Homo sapiens.
OS
FH Key
FT CDS
FT Location/Qualifiers
FT /*tag=a
FT /transl_except= "(pos: 825..827, aa: Val)"
FT /transl_except= "(pos: 1479..1481, aa: Asp)"
FT /transl_except= "(pos: 1627..1629, aa: Lys)"
FT /transl_except= "(pos: 1860..1861, aa: Ser)"
FT /transl_except= "(pos: 1968..1970, aa: Ser)"
FT /transl_except= "(pos: 2031..2033, aa: file)"
FT /transl_except= "(pos: 2088..2090, aa: Ser)"
FT /transl_except= "(pos: 2106..2108, aa: Ser)"
FT /product= "EPLIN (epithelial protein lost in neoplasm)"
XX WO200118019-A1.
XX
XX 15-MAR-2001.
XX
XX 08-SEP-2000; 2000WO-US24689.
XX
XX 08-SEP-1999; 99US-0153024.
XX (REGC) UNIV CALIFORNIA.
XX
XX Chang DD, Maul RS;
XX WPI: 2001-244555/25.
XX P-PSDB, AAB67700.
XX
XX New tumor suppressor protein EPLIN, useful as a marker for diagnostic,
XX prognostic and therapeutic applications over the course of cell
XX proliferative disorders associated with EPLIN
XX Claim 4; Page 42-43; 59pp; English.
XX
XX The present sequence encodes a human EPLIN (epithelial protein lost in
XX neoplasm)-alpha isoform. The specification also describes EPLIN-beta.
XX EPLIN is a tumor suppressor protein, whose expression is altered in
XX multiple common human tumor types. EPLIN nuclear acids and proteins are
XX used in screening assays to detect molecules that specifically bind to
XX EPLIN nuclear acids, proteins or derivatives and thus have potential use
XX as agonist or antagonist of EPLIN, in particular molecules that affect
XX cell proliferation. Thus the assays are useful for screening molecules
XX with potential utility as anticancer drugs or lead compounds for drug
XX development. EPLIN nuclear acids, proteins are useful for detecting a
XX cell proliferative disorder in a subject. EPLIN polynucleotides are
XX useful in gene therapy techniques. EPLIN is useful as a marker that
XX can be diagnostically, prognostically and therapeutically used over
XX the course of a cell proliferative disorder associated with EPLIN.
XX
XX Sequence 3543 BP; 1152 A; 711 C; 771 G; 909 T; 0 other;
SQ

Query Match 55.1%; Score 2041; DB 22; Length 3543;
Best Local Similarity 99.4%; Pred No. 0;
Matches 3371; Conservative 0; Mismatches 11; Indels 10; Gaps 3;

QY 302 AACACCGAAATCTCTCCAGCACTTTAGAAAGGGACCCCTGACTGTGTTAAAGAGAG 361
DB 159 AACACCGAAATCTCTCCAGCACTTTAGAAAGGGACCCCTGACTGTGTTAAAGAGAG 218
QY 362 TGGGAGACCCAGGCGTGGAGCAGAGTCTCACAGACTCTCTACGGAAACAGCAGCACT 421
DB 219 TGGGAGACCCAGGCGTGGAGCAGAGTCTCACAGACTCTCTACGGAAACAGCAGCACT 278
QY 422 GAGATTAGGCACAGACAGACCATCTCTGCTGAAGTGAAGTGAAGCCAGCTGCTTTGGA 481
DB 279 GAGATTAGGCACAGACAGACCATCTCTGCTGAAGTGAAGTGAAGCCAGCTGCTTTGGA 338
QY 482 GCCAAAGTGTACCAAGAGAAACAATCCACCCAGACTAGACTCAGTCACTCTCTGAA 541
DB

DB 339 GCCAAAGCTGACCAAGAGAAACAAATCCACCAGATCTTAGACTCAGGTCACTCTGTAA 398
QY 542 GCCCTCGTTCCAGGTGATATCCACATCAAGGACGGTGAGGATCTTAAAGACCACTCA 601
DB 399 GCCCTCGTTCCAGGTGATATCCACATCAAGGACGGTGAGGATCTTAAAGACCACTCA 458
QY 602 ACAGAAAGTAAAGAAATGGAATTTGTCTAGGAGATCCAGGATGAAGTAGAAAAATCA 661
DB 459 ACAGAAAGTAAAGAAATGGAATTTGTCTAGGAGATCCAGGATGAAGTAGAAAAATCA 518
QY 662 GAAATCAGTGAAGAACACAGATGCTTCGGGCNAATAGAGAAATATATATGTTCCGCTGAAC 721
DB 519 GAAATCAGTGAAGAACACAGATGCTTCGGGCNAATAGAGAAATATATATGTTCCGCTGAAC 578
QY 722 AGCTTTAAGATGATGTTTGAGAAAGTGAAACCACTCAAACTAAAGATTTCTCGGGGCCAA 781
DB 579 AGCTTTAAGATGATGTTTGAGAAAGTGAAACCACTCAAACTAAAGATTTCTCGGGGCCAA 638
QY 782 AGCCGAAGTGCAGAGTGAAGGAGATCTCTGAAACAGCTATTCTCTAGATGACCTGGAA 841
DB 639 AGCCGAAGTGCAGAGTGAAGGAGATCTCTGAAACAGCTATTCTCTAGATGACCTGGAA 698
QY 842 ATAGGCCAGGTGAGTTGTCATCTTCTACATTTGACTCGGAGAAAATAGAGTAGACGA 901
DB 699 ATAGGCCAGGTGAGTTGTCATCTTCTACATTTGACTCGGAGAAAATAGAGTAGACGA 758
QY 902 AATCTGGAATTTCCAGCGCTCTCAGAAACCTCTATAAAGGATCGAATGCCCAAGTACAG 961
DB 759 AATCTGGAATTTCCAGCGCTCTCAGAAACCTCTATAAAGGATCGAATGCCCAAGTACAG 818
QY 962 GCAGTGTGTCCAAACAAAGCAGCTCAACCAACTATACAAATGAGCTGAAAGCCAGTGT 1021
DB 819 GCAGTGTGTCCAAACAAAGCAGCTCAACCAACTATACAAATGAGCTGAAAGCCAGTGT 878
QY 1022 GCGGAAATCAAAATTCATAAATGGAGGAGAAATGTGCCCCAGGTCTCTGAGTCT 1081
DB 879 GCGGAAATCAAAATTCATAAATGGAGGAGAAATGTGCCCCAGGTCTCTGAGTCT 938
QY 1082 TGCATCACCCATCAGGAGGAGAAAGATTTCTGCAAAATGAGATAGCTTGGAGTCCGT 1141
DB 939 TGCATCACCCATCAGGAGGAGAAAGATTTCTGCAAAATGAGATAGCTTGGAGTCCGT 998
QY 1142 TCCACCCCTGCGGAAGATGACTCCC---GTCACTCCAGGTTAAGAGTGAAGTTCAACAG 1199
DB 999 TCCACCCCTGCGGAAGATGACTCCCAGGTGACTCCAGGTTAAGAGTGAAGTTCAACAG 1058
QY 1199 CTGTTCATCCCAAGCCACTAAGTCCAGATTCAGAGCCTCCAGTCTTTCTGAAAGTTCT 1258
DB 1059 CTGTTCATCCCAAGCCACTAAGTCCAGATTCAGAGCCTCCAGTCTTTCTGAAAGTTCT 1118
QY 1259 CTTCCCAAGCAATGAAGAGTTTTCAGGCACCTGCAAGAGAGACCTCGTGGAAATGTCAG 1318
DB 1119 CTTCCCAAGCAATGAAGAGTTTTCAGGCACCTGCAAGAGAGACCTCGTGGAAATGTCAG 1178
QY 1319 AAGACAGTCTATCAATGGAGCGTCTCTTGGCCAGCAGAGGTGTTTCACATCAGTGC 1378
DB 1179 AAGACAGTCTATCAATGGAGCGTCTCTTGGCCAGCAGAGGTGTTTCACATCAGTGC 1238
QY 1379 TCCGTTGCTCTTATTCGCAACCAAACTCAGTCTAGGACATATGCATCTTTACATGGA 1438
DB 1239 TCCGTTGCTCTTATTCGCAACCAAACTCAGTCTAGGACATATGCATCTTTACATGGA 1298
QY 1439 AGAATCTATTGTAAGCTCACTTCAATCAACTCTTTAAATCTAAGGCAACTATGATGA 1498
DB 1299 AGAATCTATTGTAAGCTCACTTCAATCAACTCTTTAAATCTAAGGCAACTATGATGA 1358
QY 1499 GGCTTTGGGCACAGACCAACAGAGATCTATGGGCAAGCAAAATGAAAAACGAGAGATT 1558
DB 1359 GGCTTTGGGCACAGACCAACAGAGATCTATGGGCAAGCAAAATGAAAAACGAGAGATT 1418
QY 1559 TTGGAGAGACCCAGCCAGCTTGCAAATGCAAGGAGACCCCTCAGAGCCAGGGGTAGAA 1618
DB 1419 TTGGAGAGACCCAGCCAGCTTGCAAATGCAAGGAGACCCCTCAGAGCCAGGGGTAGAA 1478

AAH18125;
26-JUN-2001 (first entry)
Human cDNA sequence SEQ ID NO:17991.
Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
Homo sapiens.
EP1074617-A2.
07-FEB-2001.
28-JUL-2000; 2000EP-0116126.
29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-018776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
(HELI-) HELIX RES INST.
Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
WPI; 2001-318749/34.
Primer sets for synthesizing polynucleotides, particularly the 5602
full-length cDNAs defined in the specification, and for the detection
and/or diagnosis of the abnormality of the proteins encoded by the
full-length cDNAs -
Claim 8; SEQ ID 17991; 2537pp + CD ROM; English.
The present invention describes primer sets for synthesising 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 3'-end sequence, where the
oligonucleotide comprises at least 15 nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
represent oligonucleotides, all of which are used in the exemplification
of the present invention.

Sequence 2207 BP; 692 A; 438 C; 512 G; 565 T; 0 other;

Query Match 41.0%; Score 1519; DB 22; Length 2207;
Best Local Similarity 99.9%; Match No. 0;
Matches 1569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1001 AATGAGCTGAAGCCAGTGGTGGCGAAATCAAAATTCATAAAATCGAGCAAAAGAGAAAT 1060
638 AATGAGCTGAAGCCAGTGGTGGCGAAATCAAAATTCATAAAATCGAGCAAAAGAGAAAT 697
1061 GTGCCCCAGTCTCTGAGTCTGATCATCCCATCAGGAAGGGGAAAGATTTCTGCAAAAT 1120
698 GTGCCCCAGTCTCTGAGTCTGATCATCCCATCAGGAAGGGGAAAGATTTCTGCAAAAT 757

QY 1121 GAGAAATAGCCTGGCAGTCCGTTCCACCCCTGCGAAGATGACTCCCGTACTCCAGGTT 1180
DB 758 GAGAAATAGCCTGGCAGTCCGTTCCACCCCTGCGAAGATGACTCCCGTACTCCAGGTT 817
QY 1181 AAGAGTGCAGGTTCAACAGCCTGTCCATCCCAAGCCACTAAGTCCAGATTCAGAGCCTCC 1240
DB 818 AAGAGTGCAGGTTCAACAGCCTGTCCATCCCAAGCCACTAAGTCCAGATTCAGAGCCTCC 877
QY 1241 AGTCTTTCTGAAAGTTTCTCCTCCCAAGCAATGAAGATTTTCAGGCACCTGCAAGAGAG 1300
DB 878 AGTCTTTCTGAAAGTTTCTCCTCCCAAGCAATGAAGATTTTCAGGCACCTGCAAGAGAG 937
QY 1301 ACTGCGTGAATGTGAGAGACAGTCTATCCAAATGGAGCGTCTCTTTGGCCAAACCCAGCAG 1360
DB 938 ACTGCGTGAATGTGAGAGACAGTCTATCCAAATGGAGCGTCTCTTTGGCCAAACCCAGCAG 997
QY 1361 GTGTTTTCAGATCAGCTCTCTGCTTCTCTATTGCAACAAACCTCAGTCTAGGAACA 1420
DB 998 GTGTTTTCAGATCAGCTCTCTGCTTCTCTATTGCAACAAACCTCAGTCTAGGAACA 1057
QY 1421 TATGCATCTTTACATGGAAGAATCTATTGTAAGCCTCACTTCAATCAACTCTTTAAATCT 1480
DB 1058 TATGCATCTTTACATGGAAGAATCTATTGTAAGCCTCACTTCAATCAACTCTTTAAATCT 1117
QY 1481 AAGGGCAACTATGATGAAGGCTTTGGGCACACACACACAGGATCTATGGCAAGCACA 1540
DB 1118 AAGGGCAACTATGATGAAGGCTTTGGGCACACACACACAGGATCTATGGCAAGCACA 1177
QY 1541 AATGAAAACGAGAGATTTTGGAGAGACAGCCAGCTTGCAAATGCAAGGAGAGACCCCT 1600
DB 1178 AATGAAAACGAGAGATTTTGGAGAGACAGCCAGCTTGCAAATGCAAGGAGAGACCCCT 1237
QY 1601 CACAGCCAGGGGTAGAAGATGCCCCCTATTGCTAAGTGGGTGCTCTGGCTCAAGTATG 1660
DB 1238 CACAGCCAGGGGTAGAAGATGCCCCCTATTGCTAAGTGGGTGCTCTGGCTCAAGTATG 1297
QY 1661 GAAGCAAGGCTCTCTCTCAGCAGAGAGAGAGACAGCCAGCTGAAACCAAGAGCTG 1720
DB 1298 GAAGCAAGGCTCTCTCTCAGCAGAGAGAGAGAGACAGCCAGCTGAAACCAAGAGCTG 1357
QY 1721 AGGATCGCTCGCCACCCCTCACTGAACTTCAGGAAGTTCAGGAAGTTCCTTGGAGAAAGG 1780
DB 1358 AGGATCGCTCGCCACCCCTCACTGAACTTCAGGAAGTTCAGGAAGTTCCTTGGAGAAAGG 1417
QY 1781 ATCAAAATGTCAAGCCCAAAATGGCTCTCTGAGAGCAAAATCAGCAAGCCCAAGTTCCT 1840
DB 1418 ATCAAAATGTCAAGCCCAAAATGGCTCTCTGAGAGCAAAATCAGCAAGCCCAAGTTCCT 1477
QY 1841 GAGGATGTCGATCTAGATCTCAAGAAAGCTAAGAGATCTCTTCACTGAAGAAAGAAC 1900
DB 1478 GAGGATGTCGATCTAGATCTCAAGAAAGCTAAGAGATCTCTTCACTGAAGAAAGAAC 1537
QY 1901 CGCCCATTCAGTGTAGCAGCTTCAATTTCAAGGACCTCTGTCAGAGAGCCCAAAACTGTG 1960
DB 1538 CGCCCATTCAGTGTAGCAGCTTCAATTTCAAGGACCTCTGTCAGAGAGCCCAAAACTGTG 1597
QY 1961 TCCCACTATCAGGAAAGGCTGGAGCATGTCAGAGCAGAGTGAAGAGTCTGTGGGTGGA 2020
DB 1598 TCCCACTATCAGGAAAGGCTGGAGCATGTCAGAGCAGAGTGAAGAGTCTGTGGGTGGA 1657
QY 2021 AGAGTTTCACAAAGGAAACAAAGTGGAAAAATGCAAGGCTTCTAAGAGAAATGGGAATGTG 2080
DB 1658 AGAGTTTCACAAAGGAAACAAAGTGGAAAAATGCAAGGCTTCTAAGAGAAATGGGAATGTG 1717
QY 2081 GGAACCAACACCTGGCAACCAACCAAGATCTTAAGGAGAGACAGGGAAGAGAAATAGGAA 2140
DB 1718 GGAACCAACACCTGGCAACCAACCAAGATCTTAAGGAGAGACAGGGAAGAGAAATAGGAA 1777
QY 2141 GGTCAATAGTTGGAGATGGAGATGAGATCTTTAGTAAGAAATGGTGCAGACTCCGATGAA 2200
DB 1778 GGTCAATAGTTGGAGATGGAGATGAGATCTTTAGTAAGAAATGGTGCAGACTCCGATGAA 1837
QY 2201 GATGATAACAGCTTCTCAACCAACCAATCTCCCAAGAACCCCAAGTCTCTGAAATGGTGC 2260

QY 1308 TGGAAATGTCAGAGACAGTCTATCCAAATGAGCGTCTCTTGGCCAAACCAGCAGGTGTTTC 1367
Db 481 TGGAAATGTCAGAGACAGTCTATCAATGAGCGTCTCTTGGCCAAACCAGCAGGTGTTTC 540
QY 1368 ACATCAGCTCTTCCGTTGCTCTATTGCAACAAACAACTCAGTCTAGGAAATATGCAAT 1427
Db 541 ACATCAGCTCTTCCGTTGCTCTATTGCAACAAACAACTCAGTCTAGGAAATATGCAAT 600
QY 1428 CTTTACATGGAAGAAATCTATTGTAAGCCTCACTTCAATCAACTCTTTAAATCTAAGGGCA 1487
Db 601 CTTTACATGGAAGAAATCTATTGTAAGCCTCACTTCAATCAACTCTTTAAATCTAAGGGCA 660
QY 1488 ACTATGATGAAGCCTTTGGGCACAGACCACACAAAGGATCTATGGCAAGCAAAATGAAA 1547
Db 661 ACTATGATGAAGCCTTTGGGCACAGACCACACAAAGGATCTATGGCAAGCAAAATGAAA 720
QY 1548 ACGAAGAGATTTTGGAGAGACAGCCAGCTTGCATAATGCAAGGGAGACCCCTCACAGCC 1607
Db 721 ACGAAGAGATTTTGGAGAGACAGCCAGCTTGCATAATGCAAGGGAGACCCCTCACAGCC 780
QY 1608 CAGGGGTAGAAGATGCCCTATTGCTAAGGTGGGTGCTCTGCTCAAGTATGGAAGCA 1667
Db 781 CAGGGGTAGAAGATGCCCTATTGCTAAGGTGGGTGCTCTGCTCAAGTATGGAAGCA 840
QY 1668 AGGCTCTCTCTCAGCAGGAGAGAGCAAGCCAGCTGAAACCAAGAGCTGAGGATCG 1727
Db 841 AGGCTCTCTCTCAGCAGGAGAGAGCAAGCCAGCTGAAACCAAGAGCTGAGGATCG 900
QY 1728 CTTGGCCACCCCTCACTGAACTTGAAGTTAGGAAGTGCCTTGGAGAAAGGATCAAAA 1787
Db 901 CTTGGCCACCCCTCACTGAACTTGAAGTTAGGAAGTGCCTTGGAGAAAGGATCAAAA 960
QY 1788 TGTCAAAGCCCCAATGGCTCTGTAAGAGCAAGCAATCAGCAAGCCCAAGTTCTGAGGATG 1847
Db 961 TGTCAAAGCCCCAATGGCTCTGTAAGAGCAAGCAATCAGCAAGCCCAAGTTCTGAGGATG 1020
QY 1848 TCGATCTAGATCTGAAGAAGCTTAAGCAGATCTTCTTCACTGAAGGAAAGAGCCGCCAT 1907
Db 1021 TCGATCTAGATCTGAAGAAGCTTAAGCAGATCTTCTTCACTGAAGGAAAGAGCCGCCAT 1080
QY 1908 TCACCTGAGCAGCTTCATTTCAAAGCACTCTGTCAAGAGCCCAAAACTGTGTCCCCAC 1967
Db 1081 TCACCTGAGCAGCTTCATTTCAAAGCACTCTGTCAAGAGCCCAAAACTGTGTCCCCAC 1140
QY 1968 CTATCAGAAAGGGTGGAGCATGTTCAGAGCAGAGTGAAGTCTGTGGTGGAAAGATTG 2027
Db 1141 CTATCAGAAAGGGTGGAGCATGTTCAGAGCAGAGTGAAGTCTGTGGTGGAAAGATTG 1200
QY 2028 CAGAAAGGAAACAAAGTGGAAATGCCAAGGCTTCTAAGAGAAATGGGAATCTGGGAA 2087
Db 1201 CAGAAAGGAAACAAAGTGGAAATGCCAAGGCTTCTAAGAGAAATGGGAATCTGGGAA 1260
QY 2088 CAACCTGGCAAAACAAAGATCTTAAAGAGAGACAGGGAAGAGAAATGAAGAGGTGATA 2147
Db 1261 CAACCTGGCAAAACAAAGATCTTAAAGAGAGACAGGGAAGAGAAATGAAGAGGTGATA 1319
QY 2148 GTTTGGAGATGGAAATCAGAAATCTTGTAGAAATGTCAGACTCCGATGAAGATGATA 2207
Db 1320 GTTTGGAGATGGAAATCAGAAATCTTGTAGAAATGTCAGACTCCGATGAAGATGATA 1379
QY 2208 ACAGCTTCTCTCAAAACAAATCTCCAAAGAACCCAGTCTCTGAATGTGTCAGTTTTG 2267
Db 1380 ACAGCTTCTCTCAAAACAAATCTCCAAAGAACCCAGTCTCTGAATGTGTCAGTTTTG 1439
QY 2268 TAGACAACACTTTGTGTGAAGATTTCACTACTCAGAAATCCAGGATGTGGAAC 2327
Db 1440 TAGACAACACTTTGTGTGAAGATTTCACTACTCAGAAATCCAGGATGTGGAAC 1499
QY 2328 TCTGGGGAGGAGAGTGGTCAAGAGCTCTCTGTGGAAGAACAGATAAAGAAATCGGT 2387
Db 1500 TCTGGGGAGGAGAGTGGTCAAGAGCTCTCTGTGGAAGAACAGATAAAGAAATCGGT 1559
QY 2388 ATTATGATGAGGATGAGGATGAAGTGAACAATTCGAATGCTGGGCCCTTAAATTC 2447

Db 1560 ATTTATGATGAGGATGAGGATGAGCAAAATGCAAAATGATGCTGGCCTTAAATTC 1619
QY 2448 TGTAGTGTAGCAGCAGCAGCTTGTGCAAAATGATGACATGAAGCAGGTATCCC 2507
Db 1620 TGTAGTGTAGCAGCAGCAGCTTGTGCAAAATGATGACATGAAGCAGGTATCCC 1679
QY 2508 AGCATGAAATGTAATTTACTTTGGAAGTAACCTTTGAAAAAGAAATTCCTTCTTAAATCAAA 2567
Db 1680 AGCATGAAATGTAATTTACTTTGGAAGTAACCTTTGAAAAAGAAATTCCTTCTTAAATCAAA 1739
QY 2568 AA 2569
Db 1740 AA 1741
RESULT 13
AAC93483
ID AAC93483 standard; cDNA; 2158 BP.
XX AC AAC93483;
XX AC
DT 16-FEB-2001 (first entry)
XX Human secreted protein gene 5 SEQ ID NO:15.
DE Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
XX antiproliferative; cytostatic; cardiac; vasotropic; cerebroprotective;
KW nontropic; neuroprotective; antibacterial; virucide; fungicide;
KW opthalmological; vulnary; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorders; cancer; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; nervous system disorder;
KW Alzheimer's disease; ocular disorder; wound healing; skin aging; ss.
XX Homo sapiens.
XX WO200061626-A1.
PN XX
XX XX
PD 19-OCT-2000.
XX XX
PF 06-APR-2000; 2000MO-US09066.
XX XX
PR 09-APR-1999; 99US-0128698.
PR 20-JAN-2000; 2000US-0176926.
XX XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX Rosen CA, Ruben SM, Komatsoulis G;
PI WPI: 2000-619227/59.
XX P-PSDB; AAB51831.
DR XX
XX New nucleic acid molecules encoding 49 human secreted proteins for
PT diagnosing, preventing or ameliorating medical conditions and used for
PT food additives or preservatives -
XX Claim 1; Page 435; 516pp; English.
CC Polynucleotide sequences AAC93479 - AAC93527 represent cDNA encoding
CC human secreted proteins AAB51827 - AAB51875. Sequences AAB51876 -
CC AAB51927 represent alternative polypeptides encoded by the genes, and
CC amino acid sequences with which they share homology. The genes and
CC proteins have activities dependent on the tissues and cells in which they
CC are expressed. Examples of their activities include immunosuppressive;
CC antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiac;
CC vasotropic; cerebroprotective; nontropic; neuroprotective; antibacterial;
CC virucide; fungicide; opthalmological; and vulnary. The secreted
CC proteins, polynucleotides, antagonists and agonists may be useful in
CC treating, preventing and/or diagnosing diseases and disorders such as
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,

angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. Oligonucleotides AAC93470 - AAC93478 and peptide AAB51826 are used in the isolation and characterization of the proteins and polynucleotides of the invention.

Sequence 2158 BP; 714 A; 383 C; 458 G; 603 T; 0 other;

Very Match 34.3%; Score 1269; DB 21; Length 2158;
t Local Similarity 99.5%; Pred. No. 0;
ches 2129; Conservative 0. Mismatches 4

1553 GAGATTTTGGAGAGACGACCCAGCTTTGCAAAATGCAAGGGAGACCCCTTCAGCGCCAGGG 1612
|||
1 GAGATTTTGGAGAGACGACCCAGCTTTGCAAAATGCAAGGGAGACCCCTTCAGCGCCAGGG 60
|||
1613 GTAGAAGATGGCCCTATTGTCTAAGGTGGGTGTCTTGCTGCAAGTATGGAAGCCAAAGGCC 1672
|||
61 GTAGAAGATGGCCCTATTGTCTAAGGTGGGTGTCTTGCTGCAAGTATGGAAGCCAAAGGCC 120
|||
1673 TCTCTTCAGCAGGAGAGGAAGACACAGCAGCTGAAACCAAGAACTGAGGATCGCCTGG 1732
|||
121 TCTCTTCAGCAGGAGAGGAAGACACAGCAGCTGAAACCAAGAACTGAGGATCGCCTGG 180
|||
1733 CCACCCCCACTGAACTTTGAAAGTTGAGGAAGTGCCTTGGAGGAGGATCAAAATGTCA 1792
|||
181 CCACCCCCACTGAACTTTGAAAGTTGAGGAAGTGCCTTGGAGGAGGATCAAAATGTCA 240
|||
1793 AAGCCCCAATGGCTCTCTGAAGACGAAATCAGCAAGCCCGAAGTTCTTGAGGATGTGGAT 1852
|||
241 AAGCCCCAATGGCTCTCTGAAGACGAAATCAGCAAGCCCGAAGTTCTTGAGGATGTGGAT 300
|||
1853 CTGATGCTGAGAGAGCTTAAGACATCTTCTTCACTGAAGAAAGAACGCCCACTTCACT 1912
|||
301 CTGATGCTGAAGAGAGCTTAAGACATCTTCTTCACTGAAGAAAGAACGCCCACTTCACT 360
|||
1913 GTACAGGCTTCATTTCAAAGCAGCTCTGTCAAGAGCCCAAAACTGTGTCCCACTATC 1972
|||
361 GTACAGGCTTCATTTCAAAGCAGCTCTGTCAAGAGCCCAAAACTGTGTCCCACTATC 420
|||
1973 AGGAAAGGCTGGAGCATGTTCAGAGCAGAGTGAAGAGTCTGTGGGTGAAGAGTTGCAGAA 2032
|||
421 AGGAAAGGCTGGAGCATGTTCAGAGCAGAGTGAAGAGTCTGTGGGTGAAGAGTTGCAGAA 480
|||
2033 AGGAAACAAGTGGAAAATGCCAGGCTTCTAAGAGAAATGGGAATGTGGGAAAACAAC 2092
|||
481 AGGAAACAAGTGGAAAATGCCAGGCTTCTAAGAGAAATGGGAATGTGGGAAAACAAC 540
|||
2093 TGGCAAAACAAGAAATCTAAGAGGAGACAGGAAGAGAGTGAAGAGTCAATGTTG 2152
|||
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2153 GAGATGGAGAAATGAGAAATCTTGTAGAAAATGGTCAGACTCCGATGAAGATCAACAGC 2212
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661 TTCTCTAAACAACAATCTCCACAAAGGAACCAAGTCTCTGAATTGGTCAGTTTGTGTA 720
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Dh	1081	CTTCATTTTACGAGTGATGATATGCATAGTCTGTGAAGCTTGTAACTGGGGAATATTT	1140
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Qy	3408	TATTTCTCAGGGTGAAATTTAAACCAACTATAGGCTTTTCTTGGGATGATTTTCTAGTCT	3467
Dh	1860	TATTTCTCAGGGTGAAATTTAAACCAACTATAGGCTTTTCTTGGGATGATTTTCTAGTCT	1919

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Db |||||
QY 3528 TGTATGATGGAGGGAGAGTGCTTTAAGCTGTAGGCTTTCTTTGTAAGTCTGATTTATA 3587
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QY 1980 TGTATGATGGAGGGAGAGTGCTTTAAGCTGTAGGCTTTCTTTGTAAGTCTGATTTATA 2039
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QY 3588 GAGATTAGCTTTAATATTTTATAGAGATGTAAGCAATCTGCTTTCTTTAGCTTTACCTA 3647
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Db |||||
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RESULT 14
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ID AAS18588 standard; cDNA; 1567 BP.
XX
AC AAS18588;
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XX
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XX
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XX
PI Li Y, Xu S, Ren S;
XX
DR WPI; 2002-011822/02.
DR P-PSDB; AAU10979.
XX
PT Cholesterol regulatory factor binding protein and its coding sequence -
XX
PS Claim 1; Page 22; 27pp; Chinese.
XX
CC The invention relates to a novel human sterol regulatory element binding
CC protein 3 (hSREBP-3) expressed in human normal hypothalamic tissue and
CC its coding sequence. Also described is the process for preparing the
CC protein and nucleic acid sequence, and the method for detecting hSREBP-3
CC nucleic acid sequence and polypeptides. The present sequence represents
CC the coding sequence of human hSREBP-3 as described in the invention.
XX
SQ Sequence 1567 BP; 513 A; 326 C; 391 G; 337 T; 0 other;
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Query Match 32.0%; Score 1186; DB 24; Length 1567;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1436; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY |||||
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QY |||||
Db 247 GAGAAATACCTGGCAGTCCGTTCCACCCCTCCGAAAGATGACTCCCGTACTCCAGGTT 306
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QY |||||
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QY |||||
Db 367 AGTCTTTCTGAAAGTCTCTCTCCCAAGCACTAAGTCCAGATTCAGAGCCTCC 426
QY |||||
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QY |||||
Db 427 ACCTGCGTGAATGTCAGAGACAGTCTATCCCAATGGAGCGTCTCTTGGCCCAAGCAG 486
QY |||||
Db 1361 GTGTTTCACATCAGTCTGTTCCGTTGCTCTATTTGCAACCAAACTCAGTCTAGGAACA 1420
QY |||||
Db 487 GTGTTTCACATCAGTCTGTTCCGTTGCTCTATTTGCAACCAAACTCAGTCTAGGAACA 546
QY |||||
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QY |||||
Db 547 TATGATCTTTTACATGGAAGATCTATTTGAAAGCTCACTTCAATCAACTTTTAAATCT 606
QY |||||
Db 1481 AAGGCCAATATGATGAAGCTTTGGGCACAGACACCAAGGATCTATGGGCAAGCAAA 1540
QY |||||
Db 607 AAGGCCAATATGATGAAGCTTTGGGCACAGACACCAAGGATCTATGGGCAAGCAAA 666
QY |||||
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QY |||||
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QY |||||
Db 1721 AGGATCGCTGGCCACCCCTCAGCTTGAAGTTCAGGAAGTCCCTTGAGGAGG 1780
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Db 1781 ATCAAAATGTCAGAAAGCCAAATGGCTCTCTGAAAGCAAAATCAGCAAGCCCAAGTTCT 1840
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QY |||||
Db 1841 GAGGATGTCGATCTAGATCTGAAGAGCTTAAGACATCTTCTTCACTGAAGAAAGAGC 1900
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Db 1901 CCCCCATTCTAGTACAGCTTCAATTTCAAGACCTCTGTCAAGAGCCCAAAACTGTG 1960
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QY |||||
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QY |||||
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QY |||||
Db 1207 GGAAGAAACAACTGGCAAGGAAACAAAGATCTTAAGAGAGAGACAGGAGAGAGAAAGTAAAGAA 1266
QY |||||

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OM nucleic - nucleic search, using sw model

Run on: January 6, 2004, 13:54:31 ; Search time 7185 Seconds
(without alignments)
12532.788 Million cell updates/sec

Title: US-09-890-549-16

Perfect score: 3705

Sequence: 1 ggcgcgggcagctaggtg.....attgaaaaaaaaaaaaaa 3705

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Database : EST.*

1: em_estba:*

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3: em_estin:*

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9: gb_est1:*

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12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

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25: em_gss_rod:*

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27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	838	22.6	1075	12	BM909158	BM909158 AGENCOURT
2	746	20.1	884	14	CD171644	CD171644 AGENCOURT
C 3	715	19.3	728	13	BU631767	BU631767 UI-H-FLO-
C 4	714	19.3	777	28	AQ314676	AQ314676 RPT111-10

5	713	19.2	785	10	BG740815	BG740815 602633701
6	695	18.8	719	14	CA412726	CA412726 UI-H-EZO-
C 7	682	18.4	745	12	CB055210	CB055210 NISC_gm08
8	677	18.3	1142	12	BM914155	BM914155 AGENCOURT
C 9	676	18.2	759	14	CA447584	CA447584 UI-H-EIO-
10	676	18.2	757	14	CB988778	CB988778 AGENCOURT
C 11	670	18.1	695	13	BU622584	BU622584 UI-H-FLI-
C 12	661	17.8	711	14	CA447848	CA447848 UI-H-EIO-
13	658	17.8	787	13	BU61039	BU61039 AGENCOURT
14	647	17.5	880	12	BI871114	BI871114 UI-H-FLI-
15	645	17.4	645	12	BM786315	BM786315 K-EST0065
C 16	644	17.4	647	14	CA432729	CA432729 UI-H-FLI-
17	639	17.2	989	12	BM552304	BM552304 AGENCOURT
18	638	17.2	781	10	BG676749	BG676749 602623316
19	638	17.2	918	13	BU850203	BU850203 AGENCOURT
C 20	637	17.2	724	12	BM980979	BM980979 UI-CF-EN1
C 21	635	17.1	647	13	BQ574891	BQ574891 UI-H-E21-
C 22	635	17.1	971	10	BE410108	BE410108 601302298
23	633	17.1	951	10	BF528886	BF528886 602043349
C 24	624	16.8	679	9	AL048162	AL048162 DAF2588K
C 25	620	16.7	725	13	BU740444	BU740444 UI-E-E01-
C 26	619	16.7	701	14	CD365699	CD365699 UI-H-F72-
C 27	618	16.7	695	14	CA420719	CA420719 UI-H-FGO-
C 28	613	16.5	767	12	BM981550	BM981550 UI-CF-EN1
C 29	611	16.5	931	12	BM449793	BM449793 AGENCOURT
C 30	606	16.4	635	14	CB050199	CB050199 NISC_g715
C 31	605	16.3	612	13	BQ632336	BQ632336 1125f12.X
C 32	589	15.9	643	12	BM999833	BM999833 UI-H-DP0-
C 33	589	15.9	643	12	BQ000468	BQ000468 UI-H-DP0-
34	586	15.8	634	10	BE729955	BE729955 601562433
C 35	585	15.8	759	12	BM977831	BM977831 UI-CF-EN1
36	584	15.8	643	13	BQ632628	BQ632628 1125f12.Y
37	582	15.7	724	14	CB055211	CB055211 NISC_gm08
38	577	15.6	1120	10	BG120125	BG120125 602153491
39	576	15.5	810	12	BM721370	BM721370 UI-E-E01-
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C 41	571	15.4	785	14	CB990409	CB990409 AGENCOURT
C 42	570	15.4	582	13	BQ772309	BQ772309 UI-H-E21-
C 43	569	15.4	582	12	BM970921	BM970921 UI-CF-EC1
C 44	566	15.3	837	13	BX365807	BX365807 8X365807
C 45	562	15.2	629	12	BQ020266	BQ020266 UI-H-E50-

ALIGNMENTS

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ACCESSION BM909158
VERSION BM909158.1 GI:19359537
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1075)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM1904 row: j column: 10
High quality sequence stop: 696.

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		/notes="Organ: brain; Vector: pOTB7; Site: 1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."	
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QY	614	AAATGGAAATTTCTAGGAGAAATCCAGGCAATGAAGTAGAAAATCAGAAATCAGTGAA	673
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DEFINITION			
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CD171644			
VERSION			
CD171644.1 GI:30852393			
KEYWORDS			
EST.			
SOURCE			
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ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 884)			
NIH-MGC http://mgi.nci.nih.gov/.			
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished			
Contact: Robert Strausberg, Ph.D.			
Email: cgabbs-remail.nih.gov			
Tissue Procurement: Dr. Michael Brownstein			
CDNA Library Preparation: Invitrogen Corp			
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)			
Clone distribution by: Agencourt Bioscience Corporation			
found through the I.M.A.G.E. Consortium/LLNL info:			
http://image.llnl.gov			
Plate: NDAM445 row: g column: 22			
High quality sequence start: 16			
High quality sequence stop: 648			
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/notes="Organ: Testis; Vector: pCMV-Sport6.1; Site 1: NotI;			
Site 2: EcoRV (destroyed); Library is oligo-dT primed and			
directionally cloned (EcoRV site is destroyed upon cloning			
). Average insert size 1.68 kb. Library was constructed by			
(Invitrogen). Note: this is a NIH_MGC Library."			
BASE COUNT			
306 a 168 c 225 g 185 t			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1730	TGGCCACCCCCCACTGAACTTGGAAAGTTGAGAAAGTTCGAGAGGATGCTTGGAGGATGATG	1789
Db	27	TGGCCACCCCCCACTGAACTTGGAAAGTTGAGAAAGTTCGAGAGGATGATG	86
QY	1790	TCAAAAGCCCAATGCGCTCTCGAAGACGAAATCAGCAAGCCGCAAGTTCCTGAGGATGTC	1849
Db	87	TCAAAAGCCCAATGCGCTCTCGAAGACGAAATCAGCAAGCCGCAAGTTCCTGAGGATGTC	146
QY	1850	GATCTAGATCTGAAAGCACTGAGAGGATCTTCTTCAAGGACCCCAAGTTCCTGAGGATGTC	1909
Db	147	GATCTAGATCTGAAAGCACTGAGAGGATCTTCTTCAAGGACCCCAAGTTCCTGAGGATGTC	206
QY	1910	ACTGTAGAGCTTCTATTTCAAGGACCCCTCTGCAAGGACCCCAAGTTCCTGAGGATGTC	1969
Db	207	ACTGTAGAGCTTCTATTTCAAGGACCCCTCTGCAAGGACCCCAAGTTCCTGAGGATGTC	266
QY	1970	ATCAGGAAGGCTGGAGATGTCAGAGCAGAGTGAAGAGTCTGTGGTGAAGAGTTGCA	2029


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RESULT 4
AQ314676/c
LOCUS
DEFINITION
  RPCI11-103F24-TV RPCI-11 Homo sapiens genomic clone RPCI-11-103F24,
  genomic survey sequence.
ACCESSION
  AQ314676
VERSION
  AQ314676.1 GI:4046139
KEYWORDS
  GSS.
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
  Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
  Use of human BAC end Sequences for Sequence-Ready Map Building
  Unpublished
  Other_GSSs: RPCI11-103F24.TJ
  Contact: Shaying Zhao, William Nierman, Mark Adams
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: hbeatigr.org
  Clones are derived from the human BAC library RPCI-11. For BAC
  library availability, please contact Pieter de Jong
  (pieter@dejong.med.buffalo.edu). Clones may be purchased from
  BACBAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
  Research Genetics (info@resgen.com). BAC end search page:
  http://www.tigr.org/tdb/hungen/bac_end_search.html
  Seq primer: T7
  Class: BAC ends.
  Location/Qualifiers
    1..777
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      /mol_type="genomic DNA"
      /db_xref="GBB:7539311"
      /db_xref="taxon:9606"
      /clone="RPCI-11-103F24"
      /sex="Male"
      /cell_type="Lymphocytes"
      /clone_lib="RPCI-11"
      /note="Vector: pBac3.6; Site_1: EcoRI; Site_2: EcoRI;
      RPCI11 Human Male BAC Library"
BASE COUNT
  164 a 199 c 139 g 275 t

Query Match
  Best Local Similarity 99.9%; Pred. No. 2.9e-164;
  Matches 764; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1775 GAAGGGATCAAAATGTCAAAAGCCCAATGGCTCTCGAAGACCAATTCAGCAAGCCCGAA 1834
1777 GAAGGGATCAAAATGTCAAAAGCCCAATGGCTCTCGAAGACCAATTCAGCAAGCCCGAA 718
1835 GTTCCTGAGGATGCGATCTAGATCTGAAGAAGCTAAGACGATCTCTTCACTGAAGGAA 1894
717 GTTCCTGAGGATGCGATCTAGATCTGAAGAAGCTAAGACGATCTCTTCACTGAAGGAA 658
1895 AGAAGCGCCCATCTACTGTAGCAGCTTCAATTCAGACACCTCTCTCAAGAGCCCAAAA 1954
657 AGAAGCGCCCATCTACTGTAGCAGCTTCAATTCAGACACCTCTCTCAAGAGCCCAAAA 598
1955 ACTGTGTCCCACTATCAGAAAGCTGAGCATGTTCAGAGCAGAGTGAAGAGTCTGTG 2014
597 ACTGTGTCCCACTATCAGAAAGCTGAGCATGTTCAGAGCAGAGTGAAGAGTCTGTG 538
2015 GTTGAAGAGTTGCAGAAAGGAAACAAAGTGGAAAATGCCAAGCTTCTTAAGAGGATGG 2074
537 GTTGAAGAGTTGCAGAAAGGAAACAAAGTGGAAAATGCCAAGCTTCTTAAGAGGATGG 478

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QY 2075 AATGTGGAAAAAACCACTGGCAAAACAAAGAAATCTAAAGGAGAGACAGGGAAGAGAGT 2134
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|
|
Db 477 AATGTGGAAAAAACCACTGGCAAAACAAAGAAATCTAAAGGAGAGACAGGGAAGAGAGT 418
|
|
|
QY 2135 AAGGAAGTCATAGTTTGGAGATGGAGAAATTTTGTAGAAAATTTGTGTCAGACTCC 2194
|
|
|
Db 417 AAGGAAGTCATAGTTTGGAGATGGAGAAATTTTGTAGAAAATTTGTGTCAGACTCC 358
|
|
|
QY 2195 GATGAAGATGATAACAGCTTCTCTCAACCAAAATCTCCACAAAGAACCAAGTCTCTGAAT 2254
|
|
|
Db 357 GATGAAGATGATAACAGCTTCTCTCAACCAAAATCTCCACAAAGAACCAAGTCTCTGAAT 298
|
|
|
QY 2255 TGGTCGAGTTTGTAGACAAACACCTTTTGTCTGAAGAATTTCTACTCTCAGAATTCAGAAATCC 2314
|
|
|
Db 297 TGGTCGAGTTTGTAGACAAACACCTTTTGTCTGAAGAATTTCTACTCTCAGAATTCAGAAATCC 238
|
|
|
C/ 2315 CAGGATGTGAACTCTCTGGAGGGGAGAAAGTGGTCAAGAGCTCTCTGTGGGAAGACAGATA 2374
|
|
|
Db 237 CAGGATGTGAACTCTCTGGAGGGGAGAAAGTGGTCAAGAGCTCTCTGTGGGAAGACAGATA 178
|
|
|
QY 2375 AAGGAAGATCGTATTATGATGAGGATGAGGATGAAGAGTGAAGAAATTTGCAATGATGCTG 2434
|
|
|
Db 177 AAGGAAGATCGTATTATGATGAGGATGAGGATGAAGAGTGAAGAAATTTGCAATGATGCTG 118
|
|
|
QY 2435 GGCCTTAATTCATGTTAGTGTAGCGAGCCACTGCGCTTTGTCAAAATGTGATGCACAT 2494
|
|
|
Db 117 GGCCTTAATTCATGTTAGTGTAGCGAGCCACTGCGCTTTGTCAAAATGTGATGCACAT 58
|
|
|
QY 2495 AAGCAGTATCCAGCATGAATGTAATTTACTTGGAAAGTAACTT 2539
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|
|
Db 57 AAGCAGTATCCAGCATGAATGTAATTTACTTGGAAAGTAACTT 13

RESULT 5
BG740815
LOCUS
DEFINITION
  602633701F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4778761 5',
  mRNA sequence.
ACCESSION
  BG740815
VERSION
  BG740815.1 GI:14051468
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  NIH-MGC http://mgi.nci.nih.gov/
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs@mail.nih.gov
  Tissue Procurement: James Cleaver, M.D.
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
  Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM10635 row: a column: 02
  High quality sequence stop: 785.
  Location/Qualifiers
    1..785
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:4778761"
      /lab_host="DH10B (T1 phage-resistant)"
      /clone_lib="NCI CGAP Skn3"
      /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
      Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
      Average insert size 1.5kb. Library constructed by Life
      Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT
  240 a 137 c 134 g 274 t

```


ORIGIN

Query Match	19.2%	Score 713	DB 10	Length 785	
Best Local Similarity	100.0%	Pred. No. 5e-164			
Matches 713	Conservative	0	Mismatches 0	Indels 0	Gaps 0
QY	2607	AGAGATAACTTTACITTAATCTCTTCATTTTACGACGTGATATGCATTAAGTCTGTAAAG	2666		
Db	1	AGAGATAACTTTACITTAATCTCTTCATTTTACGACGTGATATGCATTAAGTCTGTAAAG	60		
QY	2667	GCTTGTAAGTGGGAAATATCCACCTCATATATGCCAGATTTCTACTGTATTTCCCAAAA	2726		
Db	61	GCTTGTAAGTGGGAAATATCCACCTCATATATGCCAGATTTCTACTGTATTTCCCAAAA	120		
QY	2727	GGCAATATTAAAGTAGATAGATGATTAGTAGTATATTGTTACACACATATTTTGGAAATTAG	2786		
Db	121	GGCAATATTAAAGTAGATAGATGATTAGTAGTATATTGTTACACACATATTTTGGAAATTAG	180		
QY	2787	AGAACATACAGAAGGAATTTAGGGGCTTAAACATTAGACCTGAATGCACATTTAGTATAAA	2846		
Db	181	AGAACATACAGAAGGAATTTAGGGGCTTAAACATTAGACCTGAATGCACATTTAGTATAAA	240		
QY	2847	GGGCACAGTTGTATATTTTTTAAATGAATACCAATTTAAATTTTTTACTATTTTACCTGTGA	2906		
Db	241	GGGCACAGTTGTATATTTTTTAAATGAATACCAATTTAAATTTTTTACTATTTTACCTGTGA	300		
QY	2907	AGAGATATTTAGTCTTTAAATTTTTTAGGTTAAATTTTCTGTGTGATATATATGAGGA	2966		
Db	301	AGAGATATTTAGTCTTTAAATTTTTTAGGTTAAATTTTCTGTGTGATATATATGAGGA	360		
QY	2967	ATTTTACTACTTTATGTCTGCTCTCTAAACTACATCTGAACTCGACGCTCGTAGGTATA	3026		
Db	361	ATTTTACTACTTTATGTCTGCTCTCTAAACTACATCTGAACTCGACGCTCGTAGGTATA	420		
QY	3027	ATACAACAGAGCACCTTTTTCGAGGCAATTGAAAACCAACCTACACACTCTTCGGTGTAGA	3086		
Db	421	ATACAACAGAGCACCTTTTTCGAGGCAATTGAAAACCAACCTACACACTCTTCGGTGTAGA	480		
QY	3087	GAGATCTGCTGTCTCCAAATAAGCTTTTGATCTGCCAGTGAATTTACTGTACTCTCCAAA	3146		
Db	481	GAGATCTGCTGTCTCCAAATAAGCTTTTGATCTGCCAGTGAATTTACTGTACTCTCCAAA	540		
QY	3147	TGATTCGTTCTTTTCTGTGTGATATCTGTGCTTCTCATAAATTTACTGAAAGCTGCAATATT	3206		
Db	541	TGATTCGTTCTTTTCTGTGTGATATCTGTGCTTCTCATAAATTTACTGAAAGCTGCAATATT	600		
QY	3207	TTAGTAAATACCTTCGGGATCACTGTCCCCCATCTTCCTGTTTGTAGAGCAAAAGTGAAGGTT	3266		
Db	601	TTAGTAAATACCTTCGGGATCACTGTCCCCCATCTTCCTGTTTGTAGAGCAAAAGTGAAGGTT	660		
QY	3267	TAAAGGAGGAAGAAGAAAGAACTGCTTTACACCACTTTGAGCTCAGACCTCTAA	3319		
Db	661	TAAAGGAGGAAGAAGAAAGAACTGCTTTACACCACTTTGAGCTCAGACCTCTAA	713		

RESULT	6
CA412726/c	
LOCUS	
DEFINITION	UI-H-EZO-ban-i-17-0-UI.sl NCI-CGAP_Ch1 Homo sapiens cDNA clone EST 07-NOV-2002
ACCESSION	CA412726
VERSION	UI-H-EZO-ban-i-17-0-UI.3'
KEYWORDS	mRNA sequence.
SOURCE	EST.
ORGANISM	Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
TITLE	Tumor Gene Index
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: cgabs@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of Orthopaedics
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 1-60, >AT-rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD

[illegible]

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FEATURES
source
Location/Qualifiers
1. . 719
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue="UI-H-EZO-ban-1-17-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DHI0B (Life Technologies)"
/clone_lib="NCI CGAP Cl"
/notes="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
with a modified polylinker; Site 1: Ecor I; Site 2: Not I
NCI_CGAP_Chl is a cDNA library containing the following
tissue(s): Chondrosarcoma Grade II. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an Ecor I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCACGCT.
TAG_LIB=UI-H-EZO
TAG_TISSUE=grade-2-chondrosarcoma
TAG_SEQ=ATCTAATATG"
253 a _123 c 125 g 218 t
BASE COUNT
ORIGIN

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Query Match	18.8%	Score 695	DB 14	Length 719
Best Local Similarity	100.0%	Pred. No. 1.3e-159		
Matches 695	Conservative 0	Mismatches 0	Indels 0	Gaps 0
2998	ACATCTGAAC	TGAGCTCTCGAGTATATAACAACAGAGCAC	TTTTGAGCAATTCAA	305
719	ACATCTGAAC	TGAGCTCTCGAGTATATAACAACAGAGCAC	TTTTGAGCAATTCAA	660
3058	AAACCCACCT	TACACTCTCCGGTGCTTAGAGATCTGTGTC	TCCCAAATAGCTTTTGT	3117
659	AAACCCACCT	TACACTCTCCGGTGCTTAGAGATCTGTGTC	TCCCAAATAGCTTTTGT	600
3118	ATCTGCCAGT	GAATTACTGTACTCCAAATGATTCCTTTCTT	TCTGGTGATATCTGTGC	3177
599	ATCTGCCAGT	GAATTACTGTACTCCAAATGATTCCTTTCTT	TCTGGTGATATCTGTGC	540
3178	TTCTCATATA	TACTGAAAGCTCCAAATATTTTAGTAATAACCTTCGGGATCACTGTCC	CCCCCA	3237
539	TTCTCATATA	TACTGAAAGCTCCAAATATTTTAGTAATAACCTTCGGGATCACTGTCC	CCCCCA	480
3238	TCTTCGGTGT	TAGACAAAGTGAAGAGTTTAAAGGAGGAAGAAAGAACTGTCTTACA		3297
479	TCTTCGGTGT	TAGACAAAGTGAAGAGTTTAAAGGAGGAAGAAAGAACTGTCTTACA		420
3298	CCACTTTGAGCT	CAGACCTCTAAACCCCTGTATTTCCCTTTATGATGTCCCTTTTGTGAGACA		3357
419	CCACTTTGAGCT	CAGACCTCTCTAAACCCCTGTATTTCCCTTTATGATGTCCCTTTTGTGAGACA		360
3358	CTAATTTTTAAAT	ACTTACTAGCTCTCGAAATATATTCATTTTTATCACAGTATTCACG	3417	
359	CTAATTTTTAAAT	ACTTACTAGCTCTCGAAATATATTCATTTTTATCACAGTATTCACG	300	

Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM1999 row: k column: 09
High quality sequence stop: 678.
Location/Qualifiers
1. .1142
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5479040"
/tissue_type="astrocytoma grade IV, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 98"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
376 a 282 c 276 g 208 t

BASE COUNT 376 a 282 c 276 g 208 t
ORIGIN
Query Match 18.3%; Score 677; DB 12; Length 1142;
Best Local Similarity 99.9%; Pred. No. 2.2e-155;
Matches 727; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 347 GTGTTAAAGAGAAGTGGGAGAACCCAGGGCTGGGAGCAGAGTCTCACAGACTCTCTA 406
Db 1 GTGTTAAAGAGAAGTGGGAGAACCCAGGGCTGGGAGCAGAGTCTCACAGACTCTCTA 60
QY 407 CGGAACAGCACCTGAGATTAGGCACAGAGCAGACCATCTCTGCTGAAGTGACAAGC 466
Db 61 CGGAACAGCACCTGAGATTAGGCACAGAGCAGACCATCTCTGCTGAAGTGACAAGC 120
QY 467 CACGCTGCTTGGAGCCAAAGCTGACAAGAGAAACAAATCCACCCAGACTTACACTC 536
Db 121 CACGCTGCTTGGAGCCAAAGCTGACAAGAGAAACAAATCCACCCAGACTTACACTC 180
QY 527 AGGTCACTCTCTGAAGCCCTCGTTCAGGTCGATATCCCCACATCAAGGACGTGAGGAT 586
Db 181 AGGTCACTCTCTGAAGCCCTCGTTCAGGTCGATATCCCCACATCAAGGACGTGAGGAT 240
QY 587 CTTAAAGACCACTCAACAGAAAAGTAAAAAAATGGAAAATTTGCTAGGAGAAATCCAGGCAT 646
Db 241 CTTAAAGACCACTCAACAGAAAAGTAAAAAAATGGAAAATTTGCTAGGAGAAATCCAGGCAT 300
QY 647 GAAGTAGAAAATCAGAAATCAGTGAACACACAGATGCTTCGGGCAAAATAGAGAAATAT 706
Db 301 GAAGTAGAAAATCAGAAATCAGTGAACACACAGATGCTTCGGGCAAAATAGAGAAATAT 360
QY 707 AATGTTCCGCTGACAGGCTTAGATGATGTTTGAAGAGGTGAACCAACTCAAACTAAG 766
Db 361 AATGTTCCGCTGACAGGCTTAGATGATGTTTGAAGAGGTGAACCAACTCAAACTAAG 420
QY 767 ATTCTCCGGCCCAAGCGCAAGTGAAGTGAAGCAAGATCTCTGAAAACAGCTATTCT 826
Db 421 ATTCTCCGGCCCAAGCGCAAGTGAAGTGAAGCAAGATCTCTGAAAACAGCTATTCT 480
QY 827 CTAGATGACCTGGAATAGGCCAGGTCAGTGTGTCATCTTACATTTGACTTCGGAGAA 886
Db 481 CTAGATGACCTGGAATAGGCCAGGTCAGTGTGTCATCTTACATTTGACTTCGGAGAA 540
QY 887 AATGAGAGTAGACCAATCTGAAATCTTCCACGCTCTCAGAAACCTCTATAAGATCGA 946
Db 541 AATGAGAGTAGACCAATCTGAAATCTTCCACGCTCTCAGAAACCTCTATAAGATCGA 600

QY 947 ATGGCCAAGTACCAGGAGCTGTGTCACAAACAAAGCAGCTCAACCAACTATACAAATGAG 1006
Db 501 ATGGCCAAGTACCAGGAGCTGTGTCACAAACAAAGCAGCTCAACCAACTATACAAATGAG 660
QY 1007 CTGAAAGCCAGTGTGTCGGAATCAAAATTCATAAAATGGAGCAAAAGGAGAAATGTGCC 1066
Db 661 CTGAAAGCCAGTGTGTCGGAATCAAAATTCATAAAATGGAGCAAAAGGAGAAATGTGCC 720
QY 1067 CCAGGTCC 1074
Db 721 CCAGGTCC 728

RESULT 9
CA447584 759 bp mRNA linear EST 08-NOV-2002
LOCUS UI-H-E10-aye-b-12-0-UI.s1 NCI CGAP_E10 Homo sapiens cDNA clone
DEFINITION UI-H-E10-aye-b-12-0-UI 3', mRNA sequence.
CA447584
VERSION CA447584.1 GI:24812004
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 759)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabps@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@iowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-52, SAT rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
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1. .759
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-E10-aye-b-12-0-UI"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_E10"
/note="Organ: Left Pelvis; Vector: p7T3-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI CGAP E10 is a cDNA library containing the following
tissue(s): Chondrosarcoma. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is ACATTGCAC.
TAG LIB=UI-H-E10
TAG_TISSUE=chondrosarcoma
TAG_SEQ=ACATTGCAC"

BASE COUNT 266 a 129 c 132 g 229 t 3 others
ORIGIN
Query Match 18.2%; Score 676; DB 14; Length 759;
Best Local Similarity 99.9%; Pred. No. 5e-155;

Matches 726; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	2979	ATGTCCTGCTCTTAACATACATCCTGAACCTGACCTCTGAGGTATATAACAAGAGC	3038
Dd	730		
QY	3039	ACTTTTGGAGCAATTGAAAAACCAACCTACACTTTCGGTCTGAGAGATCTGCTGT	3098
Dd	670	ACTTTNTGAGGCAATTGAAAAACCAACCTACACTTTCGGTCTGAGAGATCTGCTGT	611
QY	3099	CTCCCAAAATAGCTTTTGATCTGCGCAGTGAATTTACTGTCTCAAAATGATTGCTTCT	3158
Dd	610	CTCCCAAAATAGCTTTTGATCTGCGCAGTGAATTTACTGTCTCAAAATGATTGCTTCT	551
QY	3159	TTTCTGCTGATATCTGCTTCTCATAATTAAGAGCTGCAATATTTAGTATACCT	3218
Dd	550		
QY	3219	TGGGATCACTGCTCCCACTCTTCCTGTTAGAGCAAGTGAAGTGAAGAGGAAG	3278
Dd	490	TGGGATCACTGCTCCCACTCTTCCTGTTAGAGCAAGTGAAGTGAAGAGGAAG	431
QY	3279	AGAAGAACTGCTTTACACCACTTGAGCTCAGACTCTAAACCCCTGATTTCCCTTATG	3338
Dd	430	AGAAGAACTGCTTTACACCACTTGAGCTCAGACTCTAAACCCCTGATTTCCCTTATG	371
QY	3339	ATGTCCTCTTTTGAGACACTTAATTTTAAATTAATTAATTAATTAATTAATTAAT	3398
Dd	370	ATGTCCTCTTTTGAGACACTTAATTTTAAATTAATTAATTAATTAATTAATTAAT	311
QY	3399	TTATCACAGTATTTCTCAGGCTGAATTTAAACCACTATAGGCTTTTCTTGGGATGAT	3458
Dd	310	TTATCACAGTATTTCTCAGGCTGAATTTAAACCACTATAGGCTTTTCTTGGGATGAT	251
QY	3459	TTCTAGTCTTAAGGTTTGGGACATTATAAACTTGAGTACATTTGTTGACACAGTTGAT	3518
Dd	250	TTCTAGTCTTAAGGTTTGGGACATTATAAACTTGAGTACATTTGTTGACACAGTTGAT	191
QY	3519	ATTCAAATTTGATGGTGGGAGGAGGTGCTTAAAGCTGTAGGCTTTTCTTTGACT	3578
Dd	190	ATTCAAATTTGATGGTGGGAGGAGGTGCTTAAAGCTGTAGGCTTTTCTTTGACT	131
QY	3579	GCATTTATAGAGATTAGCTTTAATTTTATTTATTTATTTATTTATTTATTTATTT	3638
Dd	130	GCATTTATAGAGATTAGCTTTAATTTTATTTATTTATTTATTTATTTATTTATTT	71
QY	3639	TCTACCTAGTCTGAAACATTTTATCAATAAGATTTTAAATTAATTTGAAAAAAA	3698
Dd	70	TCTACCTAGTCTGAAACATTTTATCAATAAGATTTTAAATTAATTTGAAAAAAA	11
QY	3699	AAAAAAA 3705	
Dd	10	AAAAAAA 4	

RESULT 10
CB988778
LOCUS
DEFINITION
AGENCOURT_13927895_NIH_MGC_147_Homo_sapiens_cDNA_clone
IMAGE:30341684_5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 767)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-re@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM373 row: i column: 21
High quality sequence stop: 649.

FEATURES
source
1..767
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30341684"
/tissue_type="Human Placenta"
/lab_hosts="DH10B Tona"
/clone_lib="NIH_MGC_147"
/note="Organ: placenta; Vector: pBluescriptR; Site: 1:
all-XhoI; Site: 2: BamH; Oligo-dT primed using primer
5'-TTTCTTTTCTTTTCTTTT-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein, in
(NIH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."

BASE COUNT 256 a 168 c 195 g 148 t
ORIGIN

Query Match 18.2%; Score 676; DB 14; Length 767;
Best Local Similarity 100.0%; Pred. No. 5e-155;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 AGTGTGTAGCAGCTTGGTCCGACAGGTGCGCTAGGTAGAGCCCGGACCTGTGACAGG 75
Dd 28 AGTGTGTAGCAGCTTGGTCCGACAGGTGCGCTAGGTAGAGCCCGGACCTGTGACAGG 87
QY 76 GCTGTGTAGCAGCCAGAGAAAGCGCGCTTTTAGCCAGGTATTTCACTGTCTGTAGACAA 135
Dd 88 GCTGTGTAGCAGCCAGAGAAAGCGCGCTTTTAGCCAGGTATTTCACTGTCTGTAGACAA 147
QY 136 GATGGATCATCTCCATTTAATAGACGGCAATGGACCTCACTATCATTTAGGGTAAACAG 195
Dd 148 GATGGATCATCTCCATTTAATAGACGGCAATGGACCTCACTATCATTTAGGGTAAACAG 207
QY 196 CAAAGAACTTTCTCTTGTCAACAAGAACAAAGTCATCGGCTATTTGTGAAATATTTCTCAA 255
Dd 208 CAAAGAACTTTCTCTTGTCAACAAGAACAAAGTCATCGGCTATTTGTGAAATATTTCTCAA 267
QY 256 GTACCAAGAGCAGCTGAAGAAACAAACATGGAGAGAGAGAGAGAGAGAGAGAGAGAG 315
Dd 268 GTACCAAGAGCAGCTGAAGAAACAAACATGGAGAGAGAGAGAGAGAGAGAGAGAGAG 327
QY 316 CTCCAGCAGCTTTAGAAAGGGGACCTGACTGTGTTAAAGAGAGAGAGAGAGAGAGAGAG 375
Dd 328 CTCCAGCAGCTTTAGAAAGGGGACCTGACTGTGTTAAAGAGAGAGAGAGAGAGAGAGAG 387
QY 376 GCTGGAGCAGAGTCTCACACAGACTCTCTACGGACACAGCAGCAGCTGAGATTAGGCAC 435
Dd 388 GCTGGAGCAGAGTCTCACACAGACTCTCTACGGACACAGCAGCAGCTGAGATTAGGCAC 447
QY 436 AGCAGACCATCTCTCTCTGTTGAAGTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 495
Dd 448 AGCAGACCATCTCTCTCTGTTGAAGTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 507
QY 496 AGAAGAAACAAATCCACCCAGACTCTAGACTCAGGTCACTCTCTGAAGCCCTCTGTTGAGG 555
Dd 508 AGAAGAAACAAATCCACCCAGACTCTAGACTCAGGTCACTCTCTGAAGCCCTCTGTTGAGG 567
QY 556 TCGATATCCCCACATCAAGGACCGGTGAGGATCTTAAAGACCACTCAACAGAAAGTAAAAA 615

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Db      568 TCGATATCCCATCAAGGCGGTGAGGATCTTAAAGACCCTCAACAGAAAGTAAAAA 627
QY      616 AATGAAAAATGCTTAGGAGAAATCAGGCGATCAAGTAGAAAAATCAGAAATCAGTAAAA 675
Db      628 AATGAAAAATGCTTAGGAGAAATCAGGCGATCAAGTAGAAAAATCAGTAAAA 687
QY      676 CACAGATGCTTCGGGC 691
Db      688 CACAGATGCTTCGGGC 703

RESULT 11
BU622584/c
LOCUS   BU622584      695 bp      mRNA      linear      EST 23-SEP-2002
DEFINITION
UI-H-FL1-bgc-o-10-0-UI s1 NCI CGAP_Fl1 Homo sapiens cDNA clone
UI-H-FL1-bgc-o-10-0-UI 3', mRNA sequence.
ACCESSION
VERSION  BU622584.1  GI:23288799
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 695)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clome Distribution Information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes

FEATURES
source
1..695
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FL1-bgc-o-10-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FL1"
/notes="Organ: Chondrosarcoma; Vector: pT73-Pac (Pharmacia)
with a modified polylinker; Site 1: Ecor I; Site 2: Not
I; NCI_CGAP_Fl1 is a normalized cDNA library derived from
a pool of mRNA obtained from 4 cell lines from grade III
chondrosarcoma tissues. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an Ecor I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GAGTCGGTG. The cell
lines were provided by Dr. James Martin from the
University of Iowa.
TAG_LIB=UI-H-FL1
TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
TAG_SEQ=GAGTCGGTG"

BASE COUNT  148 a  173 c  116 g  258 t
ORIGIN
Query Match      18.1%; Score 670; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.5e-153;
Matches 670; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1900 CCGCCCATTCACGTGTAGCAGCTTCATTTCAAAGCACCTCTGTCAAGAGCCCAAAAACTGT 1959
Db      683 CCGCCCATTCACGTGTAGCAGCTTCATTTCAAAGCACCTCTGTCAAGAGCCCAAAAACTGT 624
QY      1960 GTCCCACTATCAGGAAAGGCTGGAGCATGTCCAGAGCAGAGTGAAGAGTCTCTGGGTGG 2019
Db      623 GTCCCACTATCAGGAAAGGCTGGAGCATGTCCAGAGCAGAGTGAAGAGTCTCTGGGTGG 564
QY      2020 AAGAGTTTGAGAAAGGAAACAAGTGCAGAGGCTTCTTAAGAAAGATGGGAATGT 2079
Db      563 AAGAGTTTGAGAAAGGAAACAAGTGCAGAGGCTTCTTAAGAAAGATGGGAATGT 504
QY      2080 GGGAAAAACAACCTGGCAAAAACAAAGATCTAAAGGAGAGACAGGGAAGAGTAAGGA 2139
Db      503 GGGAAAAACAACCTGGCAAAAACAAAGATCTAAAGGAGAGACAGGGAAGAGTAAGGA 444
QY      2140 AGGTCTAGTTTGGAGATGGAGATGAGAAATCTTGTAGAAAATGGTGCAGACTCCGATGA 2199
Db      443 AGGTCTAGTTTGGAGATGGAGATGAGAAATCTTGTAGAAAATGGTGCAGACTCCGATGA 384
QY      2200 AGATGATACACCTTCCTCAAAACAACATCTCCACAAGAACCAAGTCTCTGAATTGGTC 2259
Db      383 AGATGATACACCTTCCTCAAAACAACATCTCCACAAGAACCAAGTCTCTGAATTGGTC 324
QY      2260 GAGTTTGTAGACAACACACCTTTTCTGAAGAAATTCACCTACTCAGAAATCAGAAATCCAGCA 2319
Db      323 GAGTTTGTAGACAACACACCTTTTCTGAAGAAATTCACCTACTCAGAAATCAGAAATCCAGCA 264
QY      2320 TGTGGAATCTCTGGAGGGAGAAAGTGGTCAAGAGAGTCTCTGTGGAGAACACAGATAAGAG 2379
Db      263 TGTGGAATCTCTGGAGGGAGAAAGTGGTCAAGAGAGTCTCTGTGGAGAACACAGATAAGAG 204
QY      2380 AAATCGGTATTATGATGAGGATGAGGATGAAGAGTGACAAATTCGAATGATGCTGGGCT 2439
Db      203 AAATCGGTATTATGATGAGGATGAGGATGAAGAGTGACAAATTCGAATGATGCTGGGCT 144
QY      2440 TAAATTCATGTTAGTGTAGCGAGCCACTGCCCTTTGTCAAAATGTATGATGCACATAAGCA 2499
Db      143 TAAATTCATGTTAGTGTAGCGAGCCACTGCCCTTTGTCAAAATGTATGATGCACATAAGCA 84
QY      2500 GGTATCCCGCAGCATGAAATGTAATTTACTTGGAGTAACCTTTGGAAAGAAATTCCTTCTTA 2559
Db      83 GGTATCCCGCAGCATGAAATGTAATTTACTTGGAGTAACCTTTGGAAAGAAATTCCTTCTTA 24
QY      2560 AAATCAAAAA 2569
Db      23 AAATCAAAAA 14

CA447848      711 bp      mRNA      linear      EST 08-NOV-2002
UI-H-B10-ayf-j-13-0-UI s1 NCI CGAP_E10 Homo sapiens cDNA clone
UI-H-B10-ayf-j-13-0-UI 3', mRNA sequence.

CA447848
VERSION  CA447848.1  GI:24812268
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 711)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

```

Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 1-52, SAT rich#Low complexity (matched complement)
Seq primer: M13 FORWARD
POLVA=Yes.

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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-E10-avf-j-13-0-UI"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP E10"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP E10 is a cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACACTTGAC.
TAG LIB=UI-H-E10
TAG_TISSUE=chondrosarcoma
TAG_SEQ=ACACTTGAC"
BASE COUNT 248 a 123 c 123 g 216 t 1 others
ORIGIN

Query Match 17.8%; Score 661; DB 14; Length 711;
Best Local Similarity 100.0%; Pred. No. 2.3e-151;
Matches 661; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3045 TGAGCAATTGAAAACCAACCTACACTCTTCGGTGCTTAGAGAGATCGTGCTGCCA 3104
DB 664 TGAGCAATTGAAAACCAACCTACACTCTTCGGTGCTTAGAGAGATCGTGCTGCCA 605
QY 3105 AATAAGCTTTGTATCTCCAGTGAATTTACTGACTCCAAATGATTCCTTTCTG 3164
DB 604 AATAAGCTTTGTATCTCCAGTGAATTTACTGACTCCAAATGATTCCTTTCTG 545
QY 3165 GTGATATCTGCTTCTCATTAATTACTGAAAGCTGCAATATTTAGTAATACCTTCGGGA 3224
DB 544 GTGATATCTGCTTCTCATTAATTACTGAAAGCTGCAATATTTAGTAATACCTTCGGGA 485
QY 3225 TCACCTGTCCCCCATCTCCGTTGTAGAGCAAGTGAAGAGTTTAAAGGAGAGAGAGAAA 3284
DB 484 TCACCTGTCCCCCATCTCCGTTGTAGAGCAAGTGAAGAGTTTAAAGGAGAGAGAGAAA 425
QY 3285 GAACGTCTTACACCACTTGAGCTCAGACCTCTTAAACCCCTGATTTCCCTTATGATGCC 3344
DB 424 GAACGTCTTACACCACTTGAGCTCAGACCTCTTAAACCCCTGATTTCCCTTATGATGCC 365
QY 3345 CCTTTTGTAGACACTAATTTTAAATCTACTAGCTCTGAAATATATGATTTTATCA 3404
DB 364 CCTTTTGTAGACACTAATTTTAAATCTACTAGCTCTGAAATATATGATTTTATCA 305
QY 3405 CAGTATCTCAGGTGAAATTTAAACCAACTATAGGCTTTTCTGGGATGATTTCTAG 3464
DB 304 CAGTATCTCAGGTGAAATTTAAACCAACTATAGGCTTTTCTGGGATGATTTCTAG 245
QY 3465 TCTTAAGGTTTGGGACATTTAAACCTTGAGTACATTTGTTACACAGTTGATTTCCA 3524
DB 244 TCTTAAGGTTTGGGACATTTAAACCTTGAGTACATTTGTTACACAGTTGATTTCCA 185
QY 3525 AATTGTATGATGGAGGGAGAGGTGCTTAAAGCTAGGCTTTTCTTGTACTGCATT 3584

Db 184 AATTGTATGATGGAGGGAGAGGTGCTTAAAGCTAGGCTTTTCTTGTACTGCATT 125
QY 3585 ATAGAGATTTAGCTTTTAAATATTTTAGAGATGTAAACACATTCTGCTTTCTTGTACTGCATT 3644
Db 124 ATAGAGATTTAGCTTTTAAATATTTTAGAGATGTAAACACATTCTGCTTTTCTTGTACTGCATT 65
QY 3645 CTAGCTCTGAACACATTTTATTTTCAATTAAGATTTTAAATTAATTTTGAATAAAAAA 3704
Db 64 CTAGCTCTGAACACATTTTATTTTCAATTAAGATTTTAAATTAATTTTGAATAAAAAA 5
QY 3705 A 3705
Db 4 A 4
RESULT 13
BU861039
LOCUS
DEFINITION BU861039 787 bp mRNA linear EST 16-OCT-2002
AGENCOURT 10436477 NIH_MGC_126 Homo sapiens cDNA clone
IMAGE:6652372 5', mRNA sequence.
BU861039
BU861039
BU861039.1 GI:24046031
EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 787)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2900 row: 1 column: 04
High quality sequence stop: 617.

FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6652372"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (Tl-phage-resistant)"
/clone_lib="NIH_MGC_126"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccgctcgcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.2%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGTGATCAACGAGATGGCCATTACGGCGGG-3' and 5'-ATTTCAGAGCGGCGGCGGCACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH_MGC_127 and NIH_MGC_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC Library."
BASE COUNT 269 a 152 c 217 g 148 t 1 others
ORIGIN
Query Match 17.8%; Score 658; DB 13; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.2e-150;

Matches 658; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		FEATURES		High quality sequence stop: 799.		
		source		Location/Qualifiers		
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Db				/organism="Homo sapiens"		
3		TGCTAAGTGGGTGCTGCTGCTCAAGTATGGAAGCCAAAGCCCTCTCTCAGCAGGAGAA 62		/mol_type="mRNA"		
QY 1690		GGAAGACAAAGCCAGCTGAAACCAAGAGAGCTGAGGATGCGCTGGCCACCCCTGAACT 1749		/db_xref="taxon:9606"		
Db				/clone="IMAGE:540454"		
63		GGAAGACAAAGCCAGCTGAAACCAAGAGAGCTGAGGATGCGCTGGCCACCCCTGAACT 122		/tissue_type="adenocarcinoma, cell line"		
QY 1750		TGAAGTTTCAGGAAGTGCCTTGGAGGAGGATCAAAAATGTCAAAGCCCAAAATGGCCTCC 1809		/lab_host="DH108 (phage-resistant)"		
Db				/clone_lib="NIH_MGC_90"		
123		TGAAGTTTCAGGAAGTGCCTTGGAGGAGGATCAAAAATGTCAAAGCCCAAAATGGCCTCC 182		/note="Organ: liver; Vector: pCMV-Sport6; Site: 1; Not1; Site: 2; SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."		
QY 1810		TGAAGACGAATCAGCAAGCCGGAAGTCTCTGAGGATGTGATCTAGATCTGAAGAAGCT 1869		BASE COUNT 308 a 136 c 181 g 255 t		
Db				ORIGIN		
183		TGAAGACGAATCAGCAAGCCGGAAGTCTCTGAGGATGTGATCTAGATCTGAAGAAGCT 242		Query Match 17.5%; Score 647; DB 12; Length 880;		
QY 1870		AAGACGATCTTCTTCACTGAAGGAAAGAACGCGCCCATTCACCTGTAGCAGCTTCATTTCA 1929		Best Local Similarity 99.9%; Pred. No. 5.1e-148;		
Db				Matches 697; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
243		AAGACGATCTTCTTCACTGAAGGAAAGAACGCGCCCATTCACCTGTAGCAGCTTCATTTCA 302		QY 2124		
QY 1930		AAGCACCTCTGTCAAGAGCCCAAAAATGTGTCTCCCACTATCAGGAAAGGCTGGAGCAT 1989		GGAAGAGAGTGAAGAAAGTCTAGCTTTGGAGATGGAGAAATGAGAAATCTTTAGAAAAATG 2183		
Db				1		
303		AAGCACCTCTGTCAAGAGCCCAAAAATGTGTCTCCCACTATCAGGAAAGGCTGGAGCAT 362		GGAAGAGAGTGAAGAAAGTCTAGCTTTGGAGATGGAGAAATGAGAAATCTTTAGAAAAATG 60		
QY 1990		GTACAGCAGCAGTGAAGAGTCTGTGGTGGAGAGTTTGCAGAAAGGAAACAACTGGAAAA 2049		QY 2184		
Db				GTGCAGACTCCGATCAAGATGATTAACAGCTTCTCTCAACCAACAAATCTCCACAAGAACCCA 2243		
363		GTACAGCAGCAGTGAAGAGTCTGTGGTGGAGAGTTTGCAGAAAGGAAACAACTGGAAAA 422		61		
QY 2050		TGCCAAGGCTTCTAAGAGAAATGGGAATGTGGGAAAAACAACTGGCAAAAACAAAGAATC 2109		GTGCAGACTCCGATCAAGATGATTAACAGCTTCTCTCAACCAACAAATCTCCACAAGAACCCA 120		
Db				2244		
423		TGCCAAGGCTTCTAAGAGAAATGGGAATGTGGGAAAAACAACTGGCAAAAACAAAGAATC 482		AGTCTCTGAATTTGGTCGAGTTTGTGAGAACACACTTTTGTCTGAAGAAATCTACTACTCAGA 2303		
QY 2110		TAAAGGAGACAGGAGGAGAGTGAAGAGTGTATAGTTTGGAGATGGAGATGAGAA 2169		121		
Db				AGTCTCTGAATTTGGTCGAGTTTGTGAGAACACACTTTTGTCTGAAGAAATCTACTACTCAGA 180		
483		TAAAGGAGACAGGAGGAGAGTGAAGAGTGTATAGTTTGGAGATGGAGATGAGAA 542		2304		
QY 2170		TCTTGTAGAAAAATGGTGCAGATCCGATGAAGATGATAACAGCTTCTCTCAACCAACATC 2229		ATCAGAAATCCCGAGATGTGGAATCTCTGGAGGGAGAAAGTGTCTCAAGAGCTCTCTGTGG 2363		
Db				181		
543		TCTTGTAGAAAAATGGTGCAGATCCGATGAAGATGATAACAGCTTCTCTCAACCAACATC 602		ATCAGAAATCCCGAGATGTGGAATCTCTGGAGGGAGAAAGTGTCTCAAGAGCTCTCTGTGG 240		
QY 2230		TCCACAAGAACCCCAAGTCTCTGAATTTGGTCGAGTTTGTAGACAAACACTTTGCTGAA 2287		2364		
Db				AAGAACAGATTAAGAGAAATCGGTATTATGATGAGGATGAGGATGAAGAGTGACAAATG 2423		
603		TCCACAAGAACCCCAAGTCTCTGAATTTGGTCGAGTTTGTAGACAAACACTTTGCTGAA 660		241		
RESULT 14				AAGAACAGATTAAGAGAAATCGGTATTATGATGAGGATGAGGATGAAGAGTGACAAATG 2423		
BI871114				2424		
LOCUS				CAATGATGCTGGGCTTAAATTCATGTTAGTGAGGAGCCACTGCCCTTTGTCAAAT 2483		
DEFINITION				301		
ACCESSION				CAATGATGCTGGGCTTAAATTCATGTTAGTGAGGAGCCACTGCCCTTTGTCAAAT 360		
VERSION				2484		
KEYWORDS				GTGATGCACATTAAGCAGGTATCCCGAGCATGAAATGTAATTTACTTGGAAAGTAACTTTGGA 2543		
SOURCE				361		
ORGANISM				GTGATGCACATTAAGCAGGTATCCCGAGCATGAAATGTAATTTACTTGGAAAGTAACTTTGGA 420		
Homo sapiens				2544		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				AAAGAATTCCTTCTTAAATCAAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAAC 2603		
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				421		
1 (bases 1 to 880)				AAAGAATTCCTTCTTAAATCAAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAAC 480		
NIH-MGC http://mgs.nci.nih.gov/ .				2604		
National Institutes of Health, Mammalian Gene Collection (MGC)				ACTAGAGATAACTTTTACTTAAATTCCTTCAATTTTAGCAGTGAATGATGATGATGATGATGATG 2663		
Unpublished				481		
Contact: Robert Strausberg, Ph.D.				ACTAGAGATAACTTTTACTTAAATTCCTTCAATTTTAGCAGTGAATGATGATGATGATGATGATG 540		
Email: cgapbs-remail.nih.gov				2664		
Tissue Procurement: ATCC				AAGCTTGTAACTGGGAAATATTCACCTGATTAATAGCCCAAGATTCTACTGTATTCCCA 2723		
cDNA Library Preparation: Life Technologies, Inc.				541		
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				AAGCTTGTAACTGGGAAATATTCACCTGATTAATAGCCCAAGATTCTACTGTATTCCCA 600		
DNA Sequencing by: Incyte Genomics, Inc.				2724		
Clone Distribution: MGC clone distribution information can be				AAAGGCAATATTAAAGGTAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2783		
found through the I.M.A.G.E. Consortium/LLNL at:				601		
http://image.llnl.gov				AAAGGCAATATTAAAGGTAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATG 660		
Plate: LLAM12030 row: f column: 23				2784		
				TAGAGAACATACAGAAGGAATTTTAGGGGCTTAAACATT 2821		
				661		
				TAGAGAACATACAGAAGGAATTTTAGGGGCTTAAACATT 698		

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LOCUS       BM786315                645 bp    mRNA    linear    EST 05-MAR-2002
DEFINITION  K-EST005015 S9SNU601 Homo sapiens cDNA clone S9SNU601-36-B02 5',
mRNA sequence.
ACCESSION   BM786315
VERSION     BM786315.1 GI:19134547
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 645)
AUTHORS     Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE       21C Frontier Korean EST Project 2001
JOURNAL     Unpublished
COMMENT     Contact: Kim YS
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Email: yongsung@mail.kribb.re.kr
Plate: 36 row: B column: 02
High quality sequence stop: 645.
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     intact mRNA was ligated with DNA-RNA linker including SfiI
     site by treatment of T4 RNA ligase and the first strand
     cDNA was synthesized with Superscript II using SfiI
     oligo-dT primer. After first strand synthesis, RNA was
     degraded by NaOH treatment and cDNA was amplified by PCR
     reaction. The PCR products were digested with SfiI and
     cloned into DraIII- digested pME18-FL3 vector. The
     obtained cDNA vectors were used for transformation of
     competent cells E. coli Top10F by electroporation method.
     The cDNA libraries constructed by this method are
     full-length enriched cDNA library."
BASE COUNT  198 a 110 c 116 g 221 t
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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SUMMARIES

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ALIGNMENTS

RESULT 1

US-09-620-312D-45
; Sequence 45, Application US/09620312D
; Patent No. 6569662

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APPLICANT:	Liu, Chenghua
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APPLICANT:	Zhou, ping
APPLICANT:	Ma, Yundqing
APPLICANT:	Wang, Dunrui
APPLICANT:	Wang, Zhiwei
APPLICANT:	John Tillinghast
APPLICANT:	Dermanac, Radomir

TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides

CURRENT APPLICATION NUMBER: US/09/620,312D

CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,300

PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 007

PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-07-21

CRICK FILING DATE: 2000-01-21
NUMBER OF SEO ID NOS: 1705

SOFTWARE: pt FL genes Version 1.0

SEQ ID NO 45

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Query Match

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US-09-016-434-680
; Sequence 680, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREMITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 680:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HNT2NOT01
; CLONE: 269891
; US-09-016-434-680

Query Match 6.7%; Score 248; DB 4; Length 413;
Best Local Similarity 100.0%; Pred. No. 4.5e-97;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1183 GAGTGAGTTCAACAGCCTGTCCATCCCAAGCAATGAAGTTTCAGGCACCTCCAGAGAGAC 1342
Db 166 GAGTGAGTTCAACAGCCTGTCCATCCCAAGCAATGAAGTTTCAGGCACCTCCAGAGAGAC 295
QY 1243 TCTTCTCAAGTTCTCTCCCAAGCAATGAAGTTTCAGGCACCTCCAGAGAGAC 1302
Db 226 TCTTCTCAAGTTCTCTCCCAAGCAATGAAGTTTCAGGCACCTCCAGAGAGAC 285
QY 1303 CTGGTGGAAATGTCAGAGACAGTCTATCCCAATGGAGCGTCTCTTTGGCCACACGAGGT 1362

Db 286 CTGGTGGAAATGTCAGAGACAGTCTATCCAAATGGAGCGTCTCTTTGGCCACACGAGGT 345
QY 1363 GTTTCACATCAGCTGCTCGTTTGGTCTCTATTGCAACAACTCAGTCTAGGACATA 1422
Db 346 GTTTCACATCAGCTGCTCGTTTGGTCTCTATTGCAACAACTCAGTCTAGGACATA 405
QY 1423 TGCATCTT 1430
Db 406 TGCATCTT 413

RESULT 5
US-09-016-434-181
; Sequence 181, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREMITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNNOT09
; CLONE: 1422786
; US-09-016-434-181

Query Match 3.2%; Score 119; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.2e-41;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2208 ACAGTTCCTCTAAACAAACAATCTCCACAGAACCCCAAGTCTCTGAATGGTCGAGTTTG 2267
Db 95 ACAGTTCCTCTAAACAAACAATCTCCACAGAACCCCAAGTCTCTGAATGGTCGAGTTTG 154
QY 2268 TAGACAAACCTTTTGTGTAAGAAATTCATCTCAGAATCAGAAATCCCGAGGATGTGGAA 2326
Db 155 TAGACAAACCTTTTGTGTAAGAAATTCATCTCAGAATCAGAAATCCCGAGGATGTGGAA 213

```
RESULT 6
US-08-937-540-7
; Sequence 7, Application US/08937540
; Patent No. 5891697
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Wise, Mitchell L
; APPLICANT: Savage, Thomas J
; APPLICANT: Katsuhira, Eva J
; TITLE OF INVENTION: Monoterpene Synthases from Common Sage
; TITLE OF INVENTION: (Salvia officinalis)
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTENSEN, O'CONNOR, JOHNSON & KINDNESS
; STREET: 1420 FIFTH AVENUE
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,540
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K
; REGISTRATION NUMBER: 26,997
; REFERENCE/DOCKET NUMBER: WSUR111254
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206 695 1718
; TELEFAX: 206 224 0779
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2022 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Salvia officinalis
; IMMEDIATE SOURCE:
; CLONE: Unknown monoterpene synthase-like sequence
; US-08-937-540-7
;
Query Match 0.6%; Score 24; DB 2; Length 2022;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3682 TAAATTTGAAAAAAGAAAAA 3705
Db 1974 TAAATTTGAAAAAAGAAAAA 1997

RESULT 7
US-07-867-106-4
; Sequence 4, Application US/07867106
; Patent No. 5389526
; GENERAL INFORMATION:
; APPLICANT: Slade, Martin B
; APPLICANT: Chang, Andy C M
; APPLICANT: Williams, Keith L
; TITLE OF INVENTION: Improved plasmid Vectors for Cellular
; TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
; STREET: One Liberty Place 46th Floor
;
Query Match 0.6%; Score 24; DB 2; Length 2022;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3682 TAAATTTGAAAAAAGAAAAA 3705
Db 1974 TAAATTTGAAAAAAGAAAAA 1997

RESULT 8
US-08-330-108-4
; Sequence 4, Application US/08330108
; Patent No. 5795752
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A.
; TITLE OF INVENTION: IL-2-Stimulated Gene
; TITLE OF INVENTION: Expression
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,108
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,736
; FILING DATE:
; APPLICATION NUMBER: US/07/796,066
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 4:
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; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/867,106
; FILING DATE: 19920625
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PJ 7187
; APPLICATION NUMBER: PCT/AU90/00530
; FILING DATE: 02-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Feeney, Joanne Longo
; REGISTRATION NUMBER: 35,134
; REFERENCE/DOCKET NUMBER: RICE-0002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3138 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-07-867-106-4
;
Query Match 0.6%; Score 24; DB 1; Length 3138;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3681 TTAAATTTGAAAAAAGAAAAA 3704
Db 2443 TTAAATTTGAAAAAAGAAAAA 2466

RESULT 8
US-08-330-108-4
; Sequence 4, Application US/08330108
; Patent No. 5795752
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A.
; TITLE OF INVENTION: IL-2-Stimulated Gene
; TITLE OF INVENTION: Expression
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,108
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,736
; FILING DATE:
; APPLICATION NUMBER: US/07/796,066
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 4:
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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: human
; CELL TYPE: T-cell blast
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: 10A8
; US-08-330-108-4

Query Match 0.6%; Score 23; DB 1; Length 199;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3683 AAAATTGAAAAA 3705
Db 177 AAAATTGAAAAA 199

RESULT 9
PCT-US92-10087-4
; Sequence 4, Application PC/TUS9210087
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A.
; TITLE OF INVENTION: IL-2-Stimulated Gene
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10087
; FILING DATE: 19921118
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/796,066
; FILING DATE: 20-NOVEMBER-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/POCKET NUMBER: DCI-028PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-227-7400
; TELEFAX: 617-227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: human
; CELL TYPE: T-cell blast
; IMMEDIATE SOURCE:
; LIBRARY:

;
; CLONE: 10A8
; PCT-US92-10087-4

Query Match 0.6%; Score 23; DB 5; Length 199;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3683 AAAATTGAAAAA 3705
Db 177 AAAATTGAAAAA 199

RESULT 10
US-09-345-468-1
; Sequence 1, Application US/09345468
; GENERAL INFORMATION:
; PATENT NO. 6245527
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2047
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-345-468-1

Query Match 0.6%; Score 23; DB 3; Length 2047;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2568 AACAAACAAAAA 2590
Db 1683 AACAAACAAAAA 1705

RESULT 11
US-09-414-453A-1
; Sequence 1, Application US/09414453A
; PATENT NO. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2047
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-414-453A-1

Query Match 0.6%; Score 23; DB 4; Length 2047;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2568 AACAAACAAAAA 2590
Db 1683 AACAAACAAAAA 1705
```

```
RESULT 12
US-09-832-312-1
; Sequence 1, Application US/09832312
; Patent No. 6548741
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-832-312-1

Query Match      0.6%; Score 23; DB 4; Length 2047;
Best Local Similarity 100.0%; Pred.No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2568 AACAAACACAAAAACACAAAAA 2590
DB 1683 AACAAACACAAAAACACAAAAA 1705

RESULT 13
US-09-276-531-8/c
; Sequence 8, Application US/09276531
; Patent No. 6183968
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lai, Freeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Reddy, Roopa
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,531
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/079,677
; FILING DATE: March 27, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lynn E. Murry, Ph.D.

; REGISTRATION NUMBER: 42,918
; REFERENCE/DOCKET NUMBER: PA-0008 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3556 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LIVRUT01
; CLONE: 1753826
US-09-276-531-8

Query Match      0.6%; Score 23; DB 3; Length 3556;
Best Local Similarity 100.0%; Pred.No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3682 TAAATTTGAAAAAAGAAAAA 3704
DB 2982 TAAATTTGAAAAAAGAAAAA 2960

RESULT 14
US-09-345-882-1/c
; Sequence 1, Application US/09345882
; Patent No. 6399373
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
; FILE REFERENCE: GENSET-031A
; CURRENT APPLICATION NUMBER: US/09/345,882
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 162450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72784
; OTHER INFORMATION: 5-124-273 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 88073
; OTHER INFORMATION: 5-127-261 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90842
; OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 93714
; OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97122
; OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97152
; OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99098
```


OTHER INFORMATION: 5-130-257	: polymorphic base A or G	FEATURE:	NAME/KEY: allele	LOCATION: 90819..90865	OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:					
LOCATION: 99117					
OTHER INFORMATION: 5-130-276	: polymorphic base A or G	FEATURE:	NAME/KEY: allele	LOCATION: 90819..90865	OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
FEATURE:					
LOCATION: 103806					
OTHER INFORMATION: 5-131-395	: polymorphic base A or T	FEATURE:	NAME/KEY: allele	LOCATION: 93690..93736	OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:					
LOCATION: 106940					
OTHER INFORMATION: 5-133-375	: polymorphic base insertion of A	FEATURE:	NAME/KEY: allele	LOCATION: 93690..93736	OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:					
LOCATION: 108106					
OTHER INFORMATION: 5-135-155	: polymorphic base insertion of A	FEATURE:	NAME/KEY: allele	LOCATION: 97099..97145	OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:					
LOCATION: 108149					
OTHER INFORMATION: 5-135-198	: polymorphic base insertion of GTTT	FEATURE:	NAME/KEY: allele	LOCATION: 97099..97145	OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:					
LOCATION: 108308					
OTHER INFORMATION: 5-135-357	: polymorphic base A or G	FEATURE:	NAME/KEY: allele	LOCATION: 97130..97177	OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:					
LOCATION: 108471					
OTHER INFORMATION: 5-136-174	: polymorphic base C or T	FEATURE:	NAME/KEY: allele	LOCATION: 97130..97177	OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:					
LOCATION: 134134					
OTHER INFORMATION: 5-140-120	: polymorphic base C or T	FEATURE:	NAME/KEY: allele	LOCATION: 99075..99121	OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:					
LOCATION: 134362					
OTHER INFORMATION: 5-140-348	: polymorphic base insertion of A	FEATURE:	NAME/KEY: allele	LOCATION: 99075..99121	OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:					
LOCATION: 134374					
OTHER INFORMATION: 5-140-361	: polymorphic base insertion of CA	FEATURE:	NAME/KEY: allele	LOCATION: 99094..99140	OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:					
LOCATION: 146328					
OTHER INFORMATION: 5-143-84	: polymorphic base A or G	FEATURE:	NAME/KEY: allele	LOCATION: 99094..99140	OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:					
LOCATION: 146345					
OTHER INFORMATION: 5-143-101	: polymorphic base A or C	FEATURE:	NAME/KEY: allele	LOCATION: 103783..103828	OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:					
LOCATION: 150329					
OTHER INFORMATION: 5-145-24	: polymorphic base A or G	FEATURE:	NAME/KEY: allele	LOCATION: 103783..103828	OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:					
LOCATION: 160031					
OTHER INFORMATION: 5-148-352	: polymorphic base G or T	FEATURE:	NAME/KEY: allele	LOCATION: 106918..106966	OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:					
LOCATION: 72771..72817					
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30					
FEATURE:					
LOCATION: 72771..72817					
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51					
FEATURE:					
LOCATION: 88050..88096					
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31					
FEATURE:					
LOCATION: 88050..88096					
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52					

NAME/KEY: allele
LOCATION: 108127...108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
NAME/KEY: allele
LOCATION: 108127...108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:

Query Match 0.6%; Score 22; DB 4; Length 162450;
Best Local Similarity 100.0%; Pred.No. 3.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2564 CAAAACACAAACAAACAAACAC 2585
DB 136286 CAAAACACAAACAAACAAACAC 136265

RESULT 15

US-08-064-694-1
Sequence 1, Application US/08064694
Patent No. 5847076
GENERAL INFORMATION:
APPLICANT: George N. DeMartino
APPLICANT: Clive A. Slaughter
APPLICANT: Patricia J. Willy
APPLICANT: Ma Chu-Ping
TITLE OF INVENTION: REGULATORS OF THE PROTEASOME
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,694
FILING DATE: 19930520
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Hodgins, Daniel S.
REGISTRATION NUMBER: 31,026
REFERENCE/DOCKET NUMBER: UTSD:356/HOD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
TELEX: No. 5847076 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-064-694-1

Query Match 0.6%; Score 21; DB 2; Length 720;
Best Local Similarity 100.0%; Pred.No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1679 CAGCAGAGAAGGAGACACAG 1699
DB 63 CAGCAGAGAAGGAGACACAG 83

Search completed: January 6, 2004, 22:10:23
Job time : 201 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2004, 16:13:06 ; Search time 1105 Seconds

(without alignments)
11605.454 Million cell updates/sec

Title: US-09-890-549-16

Perfect score: 3705

Sequence: 1 GGCgcaggagcagctagggtg.....atttgaaaaa

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2263443 seqs, 1730637950 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4526886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2565	69.2	2905	13	US-10-117-722-45
3	2565	69.2	2905	15	US-10-037-270-45
4	2130	57.5	3650	11	US-09-783-732-3
5	2041	55.1	3543	11	US-09-783-732-1
6	556	15.0	732	9	US-09-925-297-152
7	423	11.4	547	15	US-10-066-543-3200
8	415	11.2	565	15	US-10-060-036-4338
9	401	10.8	583	15	US-10-066-543-3373
10	385	10.4	698	15	US-10-198-846-10895
11	362	9.8	586	11	US-09-871-161-139
12	358	9.7	358	15	US-10-066-543-1533
13	253	6.8	262	10	US-09-796-692-2900
14	253	6.8	262	15	US-10-040-862-2900
15	212	5.7	567	15	US-10-198-846-8531

C	16	186	5.0	283	10	US-09-998-598-1767	Sequence 1767, Ap
17	175	175	4.7	175	10	US-09-878-178-2086	Sequence 2086, Ap
18	175	175	4.7	175	14	US-10-046-935-2086	Sequence 2086, Ap
19	175	175	4.7	175	15	US-10-146-935-2086	Sequence 2086, Ap
20	145	145	3.9	404	11	US-09-918-995-7225	Sequence 7225, Ap
21	140	140	3.8	518	15	US-10-198-846-1527	Sequence 1527, Ap
22	116	116	3.1	574	13	US-10-027-632-25035	Sequence 25035, A
23	116	116	3.1	574	14	US-10-027-632-25035	Sequence 25035, A
C	24	86	2.3	86	9	US-09-777-564-1052	Sequence 1052, Ap
C	25	86	2.3	86	15	US-10-015-219-1052	Sequence 1052, Ap
C	26	78	2.1	410	11	US-09-918-995-7296	Sequence 7296, Ap
C	27	73	2.0	228	10	US-09-783-590-176	Sequence 176, App
C	28	60	1.6	60	13	US-09-908-975-7077	Sequence 7077, Ap
C	29	42	1.1	840	13	US-09-865-879-3	Sequence 3, Appli
C	30	27	0.7	6334	13	US-10-311-455-1185	Sequence 1185, Ap
C	31	26	0.7	12968	13	US-10-311-455-2057	Sequence 2057, Ap
C	32	26	0.7	12968	13	US-10-240-453-297	Sequence 297, App
C	33	26	0.7	12968	15	US-10-239-676-201	Sequence 201, App
C	34	25	0.7	488	9	US-09-864-761-10140	Sequence 10140, A
C	35	25	0.7	1561	9	US-09-925-302-265	Sequence 265, App
C	36	24	0.6	552	13	US-10-027-632-248895	Sequence 248895,
C	37	24	0.6	552	14	US-10-027-632-248895	Sequence 248895,
C	38	24	0.6	793	10	US-09-878-574-4304	Sequence 4304, Ap
C	39	24	0.6	918	15	US-10-007-280A-114	Sequence 114, App
C	40	24	0.6	1593	11	US-09-764-891-9700	Sequence 9700, Ap
C	41	24	0.6	1593	15	US-10-205-428-947	Sequence 947, App
C	42	24	0.6	2753	15	US-10-007-280A-115	Sequence 115, App
C	43	24	0.6	7445	13	US-10-311-455-823	Sequence 823, App
C	44	24	0.6	17527	13	US-10-311-455-1406	Sequence 1406, Ap
C	45	23	0.6	380	15	US-10-102-524-1272	Sequence 1272, Ap

ALIGNMENTS

RESULT 1

US-09-822-849A-399
; Sequence 399, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakr
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403
; CURRENT APPLICATION NUMBER: US/09/822,849A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 399
; LENGTH: 2749
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-849A-399

Query Match 69.9%; Score 2589; DB 9; Length 2749;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2639; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1051 AAAGGAGAAATGCCCCAGGTCTTGGGTCTGCATCACCATCAGGAAGGGGAAAGAT 1110

Db 110 AAAGGAGAAATGCCCCAGGTCTTGGGTCTGCATCACCATCAGGAAGGGGAAAGAT 169

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Db 170 TTCTGCAAAATGAGAAATAGCCTGGCAGTCCGTTTCCACCCCTGCCGAAGATGACTCCCGTGA 229
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 Db 230 CTCCCGAGTTTAAAGAGTGAGGTTTCAACAGCCTGTCTCATCCCAAGCCACTAAAGTCCAGATTTC 289
 Qy 1231 CAGAGCCTCCAGTCTTTCTGAAAGTTCTCTCCCAAGCAATGAAGAGTTTTCAGGCACC 1290
 Db 290 CAGAGCCTCCAGTCTTTCTGAAAGTTCTCTCCCAAGCAATGAAGAGTTTTCAGGCACC 349
 Qy 1291 TGCAGAGAGACCTGCGTGGAACTCTCAGAGACAGTCTATCCCAATGGAGCGTCTCTTTGGC 1350
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 Qy 1351 CAACAGCAGAGTGTTCACATCAGCTGCTTCGCTTGGCTTATGCAACCAAACTCAG 1410
 Db 410 CAACAGCAGAGTGTTCACATCAGCTGCTTCGCTTGGCTTATGCAACCAAACTCAG 459
 Qy 1411 TCTAGGAACATATGCATCTTTACATGGAAGAACTCTATGTAAGCCTCACTTCAATCAACT 1470
 Db 470 TCTAGGAACATATGCATCTTTACATGGAAGAACTCTATGTAAGCCTCACTTCAATCAACT 529
 Qy 1471 CTTTAAATCTAAGGGCAACTATGATGAAGGCTTTGGGCACAGACCACACAGGATCTATG 1530
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 Qy 1531 GGCAGCAAAATGAAACGAAGAGATTTTGGAGAGACCAGCCAGCTTGCATAATGCAAG 1590
 Db 590 GGCAGCAAAATGAAACGAAGAGATTTTGGAGAGACCAGCCAGCTTGCATAATGCAAG 649
 Qy 1591 GGAGACCCCTCACAGCCCGAGGGTGAAGATGCCCCCTATTGCTAAGGTGGGTGTCCTGGC 1650
 Db 650 GGAGACCCCTCACAGCCCGAGGGTGAAGATGCCCCCTATTGCTAAGGTGGGTGTCCTGGC 709
 Qy 1651 TGCAGATGGAAGCCAGGCTCTCTCAGCAGGAGAGAGCAAGCAGCAGCTGAAAC 1710
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 Qy 1711 CAAGAAGCTGAGGATGCGCTGGCCACCCCTCACTGAACTTGGAAAGTTTCAGAAAGTGCCCT 1770
 Db 770 CAAGAAGCTGAGGATGCGCTGGCCACCCCTCACTGAACTTGGAAAGTTTCAGAAAGTGCCCT 829
 Qy 1771 GGAGGAAGGATCAAAATGTCAAAGCCCAATGGCTCTCTGAAAGCAAAATCAGCAAGCC 1830
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 Qy 1831 CGAAGTCTCAGAGATGTCATGATCTGAAAGCTAAGAGATCTCTTCACTGAA 1890
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 Qy 1891 GGAAGAGCCGCCCATTCACCTGTAGCAGCTTCACTTCAAAGCACCCTCTGTCAAGAGCCC 1950
 Db 950 GGAAGAGCCGCCCATTCACCTGTAGCAGCTTCACTTCAAAGCACCCTCTGTCAAGAGCCC 1009
 Qy 1951 AAAAACTGTGTCCCCACCTATCAGGAAAGGCTGGAGCATGTTCAGAGCAGAGTGAAGATC 2010
 Db 1010 AAAAACTGTGTCCCCACCTATCAGGAAAGGCTGGAGCATGTTCAGAGCAGAGTGAAGATC 1069
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 Db 1250 CTCCGATGAAGATGATAAGGCTTCTCAAACAACTCTCCCAAGAACCCCAAGTCTCT 1309

Qy 2251 GAATTTGGTCGAGTTTGTAGACAACACCTTTTGTGGAAGAAATTCACCTACTCAGAATCAGAA 2310
 Db 1310 GAATTTGGTCGAGTTTGTAGACAACACCTTTTGTGGAAGAAATTCACCTACTCAGAATCAGAA 1369
 Qy 2311 ATCCAGGATGTGGAACCTCTGGAGGGAGAGTGTCAAGAGCTCTCTGTGGAAGAAACA 2370
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 Qy 2371 GATAAAGAGAAATCCGTTATTATGATGAGGATGAGGATGAAAGTGCACAAATTCGAATGAT 2430
 Db 1430 GATAAAGAGAAATCCGTTATTATGATGAGGATGAGGATGAAAGTGCACAAATTCGAATGAT 1489
 Qy 2431 GCTGGCCCTTAAATTCATGTTAGTCTTAGCGAGCCACTGCCCTTTGTCAAAATGTGATGC 2490
 Db 1490 GCTGGCCCTTAAATTCATGTTAGTCTTAGCGAGCCACTGCCCTTTGTCAAAATGTGATGC 1549
 Qy 2491 ACATAGCAGGTATCCAGCATGAAATGTAATTTACTTGGAAAGTAACTTTGGAAGAAAT 2550
 Db 1550 ACATAGCAGGTATCCAGCATGAAATGTAATTTACTTGGAAAGTAACTTTGGAAGAAAT 1609
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 Db 1610 TCCTTCTTAAATCAAAACAAACAAACAAACAAACAAACAAACAAACAACTTCTAAATCTAGAG 1669
 Qy 2611 ATAACTTTACTTTAAATTTCTTCAATTTAGCAGTGAATGATATGATTAAGTCTTAAGGCTT 2670
 Db 1670 ATAACTTTACTTTAAATTTCTTCAATTTAGCAGTGAATGATATGATTAAGTCTTAAGGCTT 1729
 Qy 2671 GTAACCTGGGAAATATTCACCTGATAATAGCCAGATTTCTACTGTATTTCCCAAAGGCA 2730
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 Qy 2731 ATATTAAAGTAGATAGATGATTAGTAGTATATTGTACACACTATTTTGGAAATAGAGAA 2790
 Db 1790 ATATTAAAGTAGATAGATGATTAGTAGTATATTGTACACACTATTTTGGAAATAGAGAA 1849
 Qy 2791 CATACAGAAGGAAATTTAGGGGCTTAAACATTTACGACTGAATGCACCTTTAGTATAAGGCG 2850
 Db 1850 CATACAGAAGGAAATTTAGGGGCTTAAACATTTAGCAGTGAATGCACCTTTAGTATAAGGCG 1909
 Qy 2851 ACAGTTTGTATATTTTAAATGAATACCAATTTAAATTTTGTAGTATTTACCTGTTTAAAGAG 2910
 Db 1910 ACAGTTTGTATATTTTAAATGAATACCAATTTAAATTTTGTAGTATTTACCTGTTTAAAGAG 1969
 Qy 2911 ATTATTTAGTCTTAAATTTTGTAGTAAATTTTCTGCTGTGATATATATCAGGAATTT 2970
 Db 1970 ATTATTTAGTCTTAAATTTTGTAGTAAATTTTCTGCTGTGATATATATCAGGAATTT 2029
 Qy 2971 ACTACTTTATGCTGCTCTCTAAACATACATCTCGAACTCGAGCTCGAGGTATAATAC 3030
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 Qy 3031 AACAGAGCCTTTTGGGCAATTTGAAAAACCAACCTACACTCTTCGGTGTCTAGAGAGA 3090
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 Db 2210 TCGTTTTCTTTCTGGTGATATCTGTGCTTCTCATAAATTAAGTGAAGCTGCAATATTTTAA 2269
 Qy 3211 TAATACCTTTGGGATCACTGTCCCCCATCTTCGCTGTTAGAGCAAGTGAAGAGTTTAA 3270
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Qy 3331 CCCTTATGATGCCCTTTTGGAGACACTAAATTTTAAATACCTTACTAGCTCTGMAATAT 3390
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Qy 2390 CCCTTATGATGCCCTTTTGGAGACACTAAATTTTAAATACCTTACTAGCTCTGMAATAT 2449
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Qy 3391 ATTCAATTTTATCACAGTATTTCTCAGGGTGAATTTAAACCAACTATAGGCCCTTTTCTTG 3450
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Qy 2450 ATTGAATTTTATCACAGTATTTCTCAGGGTGAATTTAAACCAACTATAGGCCCTTTTCTTG 2509
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Qy 3451 GGATGATTTTCTAGTCTTAAGGTTTGGGACATTTAAACCTTGAATTTGTTGTATCA 3510
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Qy 2510 GGATGATTTTCTAGTCTTAAGGTTTGGGACATTTAAACCTTGAATTTGTTGTATCA 2569
Db |||||
Qy 3511 CAGTTGATATCCAAATGATCGATGGGAGGAGGTTGCTTAAAGCTGTAGGCTTTTC 3570
Db |||||
Qy 2570 CAGTTGATATCCAAATGATCGATGGGAGGAGGTTGCTTAAAGCTGTAGGCTTTTC 2629
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Qy 3571 TTTGTACTGCATTTATAGATTTAGCTTTAATATTTTATAGATCTTAAACATTTCTGC 3630
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Qy 2630 TTTGTACTGCATTTATAGATTTAGCTTTAATATTTTATAGATGTAAACATTTCTGC 2689
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Qy 3631 TTTCTTAGTCTTACCTAGTCTGAACATTTTATTTCAATAAGATTTTAAATTTG 3690
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RESULT 2

US-10-117-722-45
; Sequence 45, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219744A1ele Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2BCIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_Fl_Genes version 1.0
; SEQ ID NO 45
; LENGTH: 2905
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (173)..(2452)
US-10-117-722-45

Query Match 69.2%; Score 2565; DB 13; Length 2905;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db |||||
Qy 82 AGCAGCGCAGAGGAAAGCGCGCTTTTAGCAGGTAATTCAGTGTCTGTAGACAAGATGGA 141
Db |||||
Qy 118 AGCAGCGCAGAGGAAAGCGCGCTTTTAGCAGGTAATTCAGTGTCTGTAGACAAGATGGA 177
Db |||||
Qy 142 ATCATCTCCATTTAATAGACGGCAATGGACCTCACTATCATTTAGGGTAAACAGCCAAAGA 201
Db |||||
Qy 178 ATCATCTCCATTTAATAGACGGCAATGGACCTCACTATCATTTAGGGTAAACAGCCAAAGA 237
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Qy 202 ACTTCTCTTGTCAACAGAAACAAGTCATCGGCTATTGTGGAAATATTTCTCCAAAGTACCA 261
Db |||||
Qy 238 ACTTCTCTTGTCAACAGAAACAAGTCATCGGCTATTGTGGAAATATTTCTCCAAAGTACCA 297
Db |||||
Qy 262 GAAAGCAGCTGAAGAAACAAACATGGAAGAGAGAGTAAACACCGAAATTTCTTCCCA 321
Db |||||
Qy 298 GAAAGCAGCTGAAGAAACAAACATGGAAGAGAGAGTAAACACCGAAATTTCTTCCCA 357
Db |||||
Qy 322 GCATTTTAAAGGGGACCTTGACTGTGTTTAAAGAAAGTGGAGAACCCAGGGCTGGG 381
Db |||||
Qy 358 GCATTTTAAAGGGGACCTTGACTGTGTTTAAAGAAAGTGGAGAACCCAGGGCTGGG 417
Db |||||
Qy 382 AGCAGAGTCTCACACAGACTCTCTACGGAAACAGCAGACTCAGATTAGGCACAGACAGA 441
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Qy 418 AGCAGAGTCTCACACAGACTCTCTACGGAAACAGCAGACTCAGATTAGGCACAGACAGA 477
Db |||||
Qy 442 CCATCCTCTGCTGAAGTGACAAGCCACGCTGCTTCTGGAGCCAAAGCTGACCAAGAAGA 501
Db |||||
Qy 478 CCATCCTCTGCTGAAGTGACAAGCCACGCTGCTTCTGGAGCCAAAGCTGACCAAGAAGA 537
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Qy 502 ACAATTCACCCAGATCTAGACTCAGGTCACTCTCTGAAAGCCCTCGTTTCAAGGTCGATA 561
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Qy 562 TCCCCACATCAAGGACGCTGAGGATCTTTAAAGACCACTCAACAGAAAGTAAAAAATGGA 621
Db |||||
Qy 598 TCCCCACATCAAGGACGCTGAGGATCTTTAAAGACCACTCAACAGAAAGTAAAAAATGGA 657
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Qy 622 AAATTGCTAGAGAAATCCAGGCATGAAGTAGAAAAATCAGAAATCAGTGAACACACAGA 681
Db |||||
Qy 658 AAATTGCTAGAGAAATCCAGGCATGAAGTAGAAAAATCAGAAATCAGTGAACACACAGA 717
Db |||||
Qy 682 TGTTCGGGCAAAATAGAGAAATATAATTTCCGCTGAACAGGCTTAAGATGATGTTGA 741
Db |||||
Qy 718 TGTTCGGGCAAAATAGAGAAATATAATTTCCGCTGAACAGGCTTAAGATGATGTTGA 777
Db |||||
Qy 742 GAAAGGTGAACCAACTCAAACTAAGATTTCTCGGCGCCCAAGCCGAGTGAAGTGAAG 801
Db |||||
Qy 778 GAAAGGTGAACCAACTCAAACTAAGATTTCTCGGCGCCCAAGCCGAGTGAAGTGAAG 837
Db |||||
Qy 802 GAAGATCTCTGAACACAGCTATTCTCTAGATGACTGGAATAGGCCAGGTCAGTTCGTC 861
Db |||||
Qy 838 GAAGATCTCTGAACACAGCTATTCTCTAGATGACTGGAATAGGCCAGGTCAGTTCGTC 897
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Qy 862 ATCTTCTACATTTGACTCGGAGAAAAATGAGAGTAGACGAAATCTGGAACCTTCCACGCT 921
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Qy 898 ATCTTCTACATTTGACTCGGAGAAAAATGAGAGTAGACGAAATCTGGAACCTTCCACGCT 957
Db |||||
Qy 922 CTCAGAAACCTCTATAAAGGATCGAATGGCCAAAGTACCAGGCAGCTGTGTCCAAACAAAG 981
Db |||||
Qy 958 CTCAGAAACCTCTATAAAGGATCGAATGGCCAAAGTACCAGGCAGCTGTGTCCAAACAAAG 1017
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Qy 982 CAGCTCAACCAACTATAAATGAGCTGAAAGCCAGTGGTGGCGAAATCAAAATTCATAA 1041
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Qy 1018 CAGCTCAACCAACTATAAATGAGCTGAAAGCCAGTGGTGGCGAAATCAAAATTCATAA 1077
Db |||||
Qy 1042 AATGAGCAAAAGGAGATGTGCCCCAGGTCCTGAGGTCTGCATCACCCTCAGGAGG 1101
Db |||||
Qy 1078 AATGAGCAAAAGGAGATGTGCCCCAGGTCCTGAGGTCTGCATCACCCTCAGGAGG 1137
Db |||||
Qy 1102 GGAAGAAGATTTCTGCAATGAGATAGCTGGCAGTCGTTCCACCCCTGCGGAGATGA 1161
Db |||||
Qy 1138 GGAAGAAGATTTCTGCAATGAGATAGCTGGCAGTCGTTCCACCCCTGCGGAGATGA 1197
Db |||||
Qy 1162 CTCCTGCTGACTCCAGGTTAAGAGTGAAGTTCAACAGGCTGTCCATCCCAAGCCACTAAG 1221
Db |||||
Qy 1198 CTCCTGCTGACTCCAGGTTAAGAGTGAAGTTCAACAGGCTGTCCATCCCAAGCCACTAAG 1257
Db |||||
Qy 1222 TCCAGATTCGAGGCTCCAGTCTTTTGAAGTTTCTCTCCCAAGCAATGAAGAAATT 1281
Db |||||
Qy 1258 TCCAGATTCGAGGCTCCAGTCTTTTGAAGTTTCTCTCCCAAGCAATGAAGAAATT 1317
Db |||||
Qy 1282 TCAGGCACCTCGAAGAGACCTCGCTGGAATGTTCAGNAGACAGTCTTCAATGGAGCG 1341
Db |||||

Db 1318 TCAGGCACCTGCAAGAGAGACCTGCGTGGAAATGTCAGAAACAGCTCTATCAATGGAGCG 1377
Qy 1342 TCTCTGGCCAAACAGCAGAGTGTTTCACATCAGCTGCTTCGCTGCTCTATGCAACAA 1401
Db 1378 TCTCTGGCCAAACAGCAGAGTGTTTCACATCAGCTGCTTCGCTGCTCTATGCAACAA 1437
Qy 1402 CAAACTCAGTCTAGGAACATATGCACTTTTACATGGAAGAAATCTATTTGAAGCTCACTT 1461
Db 1438 CAAACTCAGTCTAGGAACATATGCACTTTTACATGGAAGAAATCTATTTGAAGCTCACTT 1497
Qy 1462 CAATCAACTCTTTAAATCTAAGGCAACTATGATGAAGCTTTGGGCACAGCACACAA 1521
Db 1498 CAATCAACTCTTTAAATCTAAGGCAACTATGATGAAGCTTTGGGCACAGCACACAA 1557
Qy 1522 GGATCTATGGCCAGCAAGCAAAATGAAACGAAAGATTTTGGAGAGACAGCCAGCTTGC 1581
Db 1558 GGATCTATGGCCAGCAAGCAAAATGAAACGAAAGATTTTGGAGAGACAGCCAGCTTGC 1617
Qy 1582 AAATGCAAGGAGAGACCCCTCACAGCCAGGGGTAGAAAGTCCCTTATTTGCTAAGGTGGG 1641
Db 1618 AAATGCAAGGAGAGACCCCTCACAGCCAGGGGTAGAAAGTCCCTTATTTGCTAAGGTGGG 1677
Qy 1642 TGTCTGCTGCAAGTATGGAAGCCAGGCTCTCTCAGCAGGAGAGGAAGCAAGCC 1701
Db 1678 TGTCTGCTGCAAGTATGGAAGCCAGGCTCTCTCAGCAGGAGAGGAAGCAAGCC 1737
Qy 1702 AGCTGAACCCAGAGCTGAGATCGCTGCGCACCCCTCACTGAAGTTCAGG 1761
Db 1738 AGCTGAACCCAGAGCTGAGATCGCTGCGCACCCCTCACTGAAGTTCAGG 1797
Qy 1762 AAGTCCCTTGGAGGAAGGATCAAAATGTCAAAGCCCAAAATGGCTCTGGAAGCAGAAAT 1821
Db 1798 AAGTCCCTTGGAGGAAGGATCAAAATGTCAAAGCCCAAAATGGCTCTGGAAGCAGAAAT 1857
Qy 1822 CAGCAAGCCCGAAGTTCCTGAGGATGTGATCTAGATCTGAAGAGCTTAAGCATCTTC 1881
Db 1858 CAGCAAGCCCGAAGTTCCTGAGGATGTGATCTAGATCTGAAGAGCTTAAGCATCTTC 1917
Qy 1882 TTCACTGAAGGAAGCAAGCCCGCAATTCACCTGTAGCAGCTTCATTTCAAGCAGCTCTGT 1941
Db 1918 TTCACTGAAGGAAGCAAGCCCGCAATTCACCTGTAGCAGCTTCATTTCAAGCAGCTCTGT 1977
Qy 1942 CAAGAGCCCAAAATGTGTCTCCCACTTATCAGGAAGGCTGGAGCATGTGAGAGCAGAG 2001
Db 1978 CAAGAGCCCAAAATGTGTCTCCCACTTATCAGGAAGGCTGGAGCATGTGAGAGCAGAG 2037
Qy 2002 TGAAGAGTCTGTGGTGGAGAGTTGCAAGAAAGAAACAAGTGGAAAAATGCCAGGCTTC 2061
Db 2038 TGAAGAGTCTGTGGTGGAGAGTTGCAAGAAAGAAACAAGTGGAAAAATGCCAGGCTTC 2097
Qy 2062 TAAGAGAAATGGAAATGTGGGAAAAACAACCTGGCAAAACAAGAAATCTAAGAGGAGAC 2121
Db 2098 TAAGAGAAATGGAAATGTGGGAAAAACAACCTGGCAAAACAAGAAATCTAAGAGGAGAC 2157
Qy 2122 AGGGAAGAGAACTAAGGAAGTCAATGTTTGGAGATGGAGATGAGAAATCTGTAGAAAA 2181
Db 2158 AGGGAAGAGAACTAAGGAAGTCAATGTTTGGAGATGGAGATGAGAAATCTGTAGAAAA 2217
Qy 2182 TGGTGCAGACTCCGATGAAGATGATAACAGCTTCTCAAACAACAAATCTCCACAGAAC 2241
Db 2218 TGGTGCAGACTCCGATGAAGATGATAACAGCTTCTCAAACAACAAATCTCCACAGAAC 2277
Qy 2242 CAACTCTCTGAATTTGGTCAAGTTTTGTAGACAACACCTTTGCTGAAGAAATTCACCTCA 2301
Db 2278 CAACTCTCTGAATTTGGTCAAGTTTTGTAGACAACACCTTTGCTGAAGAAATTCACCTCA 2337
Qy 2302 GAATCAGAAATCCAGGATGTGGAATCTGGGAGGAGAGTGGTCAAGAGCTCTCTGT 2361
Db 2338 GAATCAGAAATCCAGGATGTGGAATCTGGGAGGAGAGTGGTCAAGAGCTCTCTGT 2397
Qy 2362 GGAAGAACAGATAAGAGAAATCGGTATTTATGATGAGATGAGGATGAGAGTGAACAAAT 2421

Db 2398 GGAAGAACAGATAAGAGAAATCGGTATTATGATGAGCATGAGGATGAAGATGACAAAT 2457
Qy 2422 TCCAATGATGCTGGGCCCTTAAATTCATGTTAGTGTAGCGAGCCACTGCCCTTTGTCAAA 2481
Db 2458 TCCAATGATGCTGGGCCCTTAAATTCATGTTAGTGTAGCGAGCCACTGCCCTTTGTCAAA 2517
Qy 2482 ATGTGATGCACATAGCAGGATATCCAGCATGAATTTACTTTGGAAGTAACTTTG 2541
Db 2518 ATGTGATGCACATAGCAGGATATCCAGCATGAATTTACTTTGGAAGTAACTTTG 2577
Qy 2542 GAAAGAAATTCCTTCTTAAATCAAAAACAAAACAAAACAAAACAAAACACA 2586
Db 2578 GAAAGAAATTCCTTCTTAAATCAAAAACAAAACAAAACAAAACAAAACACA 2622

RESULT 3
US-10-037-270-45
; Sequence 45, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Felyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1e1 Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt.Fl_genes Version 1.0
; SEQ ID NO 45
; LENGTH: 2905
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (173)..(2452)
US-10-037-270-45

Query Match 69.2%; Score 2565; DB 15; Length 2905;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TAGCAGCTTGGTCCGACAGGTGCGCTAGGTAGAGCGCCGGGACCTGTGACAGGGCTGGT 81
Db 58 TAGCAGCTTGGTCCGACAGGTGCGCTAGGTAGAGCGCCGGGACCTGTGACAGGGCTGGT 117
Qy 82 AGCAGCGCAGAGGAAAGCGCGCTTTTAGCCAGGTATTTAGTGTCTGTAGACAAGATGGA 141
Db 118 AGCAGCGCAGAGGAAAGCGCGCTTTTAGCCAGGTATTTAGTGTCTGTAGACAAGATGGA 177
Qy 142 ATCATCTCCATTTAATAGACGGCAATGGACCTCACTATCATTTAGGGGTAAACAGCCAAAGA 201
Db 178 ATCATCTCCATTTAATAGACGGCAATGGACCTCACTATCATTTAGGGGTAAACAGCCAAAGA 237

y	202	ACTTTTCTCTTGTCAACAAGAA	CAAGTCATCGGCTATTGTGGA	AATATTCTTCCAAGTACCA	261
b	238	ACTTTTCTCTTGTCAACAAGAA	CAAGTCATCGGCTATTGTGGA	AATATTCTTCCAAGTACCA	297
y	262	GAAACAGCTGAAGAAACAA	CATCGAGAAGAGAGTA	ACACGGAATCTCTCCCA	321
b	298	GAAACAGCTGAAGAAACAA	CATCGAGAAGAGAGTA	ACACGGAATCTCTCCCA	357
y	322	GCACITTTAGAAGGGACCC	TGACTGTGTTAAAGAAAGT	GGGAGAACCCAGGGCTGGG	381
b	358	GCACITTTAGAAGGGACCC	TGACTGTGTTAAAGAAAGT	GGGAGAACCCAGGGCTGGG	417
y	382	AGCAGAGTCTCACACAGAT	CTCTACGGACACAGCACT	GAGATTAGGCACAGACAGA	441
b	418	AGCAGAGTCTCACACAGAT	CTCTACGGACACAGCACT	GAGATTAGGCACAGACAGA	477
y	442	CAATCTCTGCTGAAGTGA	CAAGCCACGCTGCTTCT	GGAGCCAAAGCTGACCAAGAG	501
b	478	CAATCTCTGCTGAAGTGA	CAAGCCACGCTGCTTCT	GGAGCCAAAGCTGACCAAGAG	537
y	502	ACAAATCCACCCACAGAT	CTAGACTCAGGTCACCT	CCTGAAAGCCCTCGTTCAGGGTCGATA	561
b	538	ACAAATCCACCCACAGAT	CTAGACTCAGGTCACCT	CCTGAAAGCCCTCGTTCAGGGTCGATA	597
y	562	TCCCAACATCAAGGACG	TGAGGATCTTAAAGACACT	CAACAGAAAGTAAAAAATGGA	621
b	598	TCCCAACATCAAGGACG	TGAGGATCTTAAAGACACT	CAACAGAAAGTAAAAAATGGA	657
y	622	AAATTGCTAGAGAGAT	CCAGGCATGAAGTAGA	AAATCAGAAATCAGTGAAACACAGA	681
b	658	AAATTGCTAGAGAGAT	CCAGGCATGAAGTAGA	AAATCAGAAATCAGTGAAACACAGA	717
y	682	TGCTTCGGGCAAAATAG	AGAAATATAATGTTCCG	CTGAACAGGCTTAAAGATGATTTGA	741
b	718	TGCTTCGGGCAAAATAG	AGAAATATAATGTTCCG	CTGAACAGGCTTAAAGATGATTTGA	777
y	742	GAAAGGTGAACCAACT	CAAACTAAGATTTCT	CGGGCCCAAGCCGAAAGTGAAG	801
b	778	GAAAGGTGAACCAACT	CAAACTAAGATTTCT	CGGGCCCAAGCCGAAAGTGAAG	837
y	802	GAAAGATCTCTGAAAAC	AGCTATTCTCTAGATGAC	CTGGAATAGGCCAGGTCAGTTGTC	861
b	838	GAAAGATCTCTGAAAAC	AGCTATTCTCTAGATGAC	CTGGAATAGGCCAGGTCAGTTGTC	897
y	862	ATCTTCTACATTTGACT	CGGAGAAAATGAGATG	ACGAAATCTGGAACCTTCCACGCCCT	921
b	898	ATCTTCTACATTTGACT	CGGAGAAAATGAGATG	ACGAAATCTGGAACCTTCCACGCCCT	957
y	922	CTCAGAAACCTCTATA	AAAGGATCGAATGGCCAA	AGTACCAGGCAGCTGTGTCCAAACAAAG	981
b	958	CTCAGAAACCTCTATA	AAAGGATCGAATGGCCAA	AGTACCAGGCAGCTGTGTCCAAACAAAG	1017
y	982	CAGCTCAACCAACTAT	ACAAATGAGCTGAA	AGCCAGTGTGGCGAAATCAAAATTCATAA	1041
b	1018	CAGCTCAACCAACTAT	ACAAATGAGCTGAA	AGCCAGTGTGGCGAAATCAAAATTCATAA	1077
y	1042	AATGGAGCAAAAGGAG	AAATGCCCCAGGTCCT	CAGGTCGTGCATCACCCATCAGGAAG	1101
b	1078	AATGGAGCAAAAGGAG	AAATGCCCCAGGTCCT	CAGGTCGTGCATCACCCATCAGGAAG	1137
y	1102	GGAAAAAGATTTCTG	CAAAATGAGATAGCCT	GGCAGTCCGTTCCACCCCTGCCGAAGATGA	1161
b	1138	GGAAAAAGATTTCTG	CAAAATGAGATAGCCT	GGCAGTCCGTTCCACCCCTGCCGAAGATGA	1197
y	1162	CTCCCGTGACTCCCA	GGTTAAGAGTGA	GGTTCAACAGCCTGTCCATCCCAAGCCACTAAG	1221
b	1198	CTCCCGTGACTCCCA	GGTTAAGAGTGA	GGTTCAACAGCCTGTCCATCCCAAGCCACTAAG	1257
y	1222	TCCAGATTCAGAGCCT	CCAGTCTTTCTGAAAGT	TCTCCTCCCAAGCAATGAAGAAGTT	1281
b	1258	TCCAGATTCAGAGCCT	CCAGTCTTTCTGAAAGT	TCTCCTCCCAAGCAATGAAGAAGTT	1317
y	1282	TCAGGCACCTGCA	AGAGACCTGCGTGA	ATCTCAGAAAGACAGTCTATCCAAATGGAGCG	1341

1318	TC	AGGCACCTGCAAGAGAGACCTCGGTGGAAATGTGAGAACACAGTCTATCCAAATGGAGCG	1377
1342	TC	CTTTGGCCCAACCAAGCAGAGGTGTTTTCACATCAGCTGCTTCOGTTGCTCCTATTGCAACAA	1401
1378	TC	CTTTGGCCCAACCAAGCAGAGGTGTTTTCACATCAGCTGCTTCOGTTGCTCCTATTGCAACAA	1437
1402	CAAA	CTCAGTCTAGGAAACATATGCATCTTTACATTTGGAAGAAATCTATTGTAAGGCTCACTT	1461
1438	CAAA	CTCAGTCTAGGAAACATATGCATCTTTACATTTGGAAGAAATCTATTGTAAGGCTCACTT	1497
1462	CAAT	CAACTCTTTAAATCTAAGGGCAACTATGATGAAGGCTTTTGGGCACAGACACACAA	1521
1498	CAAT	CAACTCTTTAAATCTAAGGGCAACTATGATGAAGGCTTTTGGGCACAGACACACAA	1557
1522	GGAT	CTATGGGCAAGCAAAATGAAACGAAAGATTTTGAGAGACACAGCCAGCTTGC	1581
1558	GGAT	CTATGGGCAAGCAAAATGAAACGAAAGATTTTGAGAGACACAGCCAGCTTGC	1617
1582	AAAT	GCAAGGGAGACCCCTCACAGCCAGGGGTAGAAGATGCCCTATTGCTAAGGTGGG	1641
1618	AAAT	GCAAGGGAGACCCCTCACAGCCAGGGGTAGAAGATGCCCTATTGCTAAGGTGGG	1677
1642	TGTC	TGGCTGCAAGTATGGAAGCCAAAGGCTCTCTCTCAGCAGGAGAGGAAGACAAGCC	1701
1678	TGTC	TGGCTGCAAGTATGGAAGCCAAAGGCTCTCTCTCAGCAGGAGAGGAAGACAAGCC	1737
1702	AGCT	GAAACCAAGAAAGCTGAGGATCGCTGGCCACCCCACTGAACTTGAAGTTCAAG	1761
1738	AGCT	GAAACCAAGAAAGCTGAGGATCGCTGGCCACCCCACTGAACTTGAAGTTCAAG	1797
1762	AAGT	GGCTTTGGAGGAAGGGATCAAAATGTCAAAGCCCAAAATGGGCTCTCTGAAGACGAAAT	1821
1798	AAGT	GGCTTTGGAGGAAGGGATCAAAATGTCAAAGCCCAAAATGGGCTCTCTGAAGACGAAAT	1857
1822	CAGC	AAAGCCGGAAGTTCTGAGGATGTGATCTAGATCTGAAGAGAGCTTAAGACGATCTTC	1881
1858	CAGC	AAAGCCGGAAGTTCTGAGGATGTGATCTAGATCTGAAGAGAGCTTAAGACGATCTTC	1917
1882	TTCA	CTGAAGGAAAGAGCGGCCCAATTCACGTAGCAGCTTCATTTCAAAGCACTCTGT	1941
1918	TTCA	CTGAAGGAAAGAGCGGCCCAATTCACGTAGCAGCTTCATTTCAAAGCACTCTGT	1977
1942	CAAG	AGCCCAAAACCTGTGTCCCACTTCATCAGGAAAGGCTGGAGCATGTGAGAGCAGAG	2001
1978	CAAG	AGCCCAAAACCTGTGTCCCACTTCATCAGGAAAGGCTGGAGCATGTGAGAGCAGAG	2037
2002	TGA	GAGTCTGTGGTGGAAAGAGTTCGAAAGGAAACAAAGTGGAAATGCCAAGGCTTC	2061
2038	TGA	GAGTCTGTGGTGGAAAGAGTTCGAAAGGAAACAAAGTGGAAATGCCAAGGCTTC	2097
2062	TAAG	AGAAATGGGAATGTGGGAAACAAACCTGGCAAAAGAAATCTTAAGGAGAGAC	2121
2098	TAAG	AGAAATGGGAATGTGGGAAACAAACCTGGCAAAAGAAATCTTAAGGAGAGAC	2157
2122	AGGA	AGAGAAATGAAGGAAGGTCATAGTTTGAGATGGGAATGAGAAATCTTTAGAAAA	2181
2158	AGGA	AGAGAAATGAAGGAAGGTCATAGTTTGAGATGGGAATGAGAAATCTTTAGAAAA	2217
2182	TGGT	GAGACTCCGATGAAGATGATAACAGCTTCTCAAAACAACATCTCCACAAGAAC	2241
2218	TGGT	GAGACTCCGATGAAGATGATAACAGCTTCTCCAAAACAACATCTCCACAAGAAC	2277
2242	CAAG	TCTCTGAATTTGGTTCAGTTTGTAGACAACACCTTTGCTGAGAAATTCACCTACTCA	2301
2278	CAAG	TCTCTGAATTTGGTTCAGTTTGTAGACAACACCTTTGCTGAGAAATTCACCTACTCA	2337
2302	GAAT	CAGAAATCCAGGATGTGGAATCTCTGGAGGGAGAGTGGTCAAGAGACTCTCTGT	2361
2338	GAAT	CAGAAATCCAGGATGTGGAATCTCTGGAGGGAGAGTGGTCAAGAGACTCTCTGT	2397
2362	GGAA	GAACACAGATTAAGAGAAATTCGGTATTATGATGAGGATGAGGATGAAGAGTGCACAAAT	2421

Db 2398 GGAAGAACAGATAAAGAGAAATCGGTATTATGATGAGGATGAGGATGAAGAGTGACAAAT 2457
QY 2422 TGCATATGCTGGGCTTTAAATTCATGTTACTGTTAGCGCCACTGCCCTTTGTCAAA 2481
Db 2458 TGCATATGCTGGGCTTTAAATTCATGTTACTGTTAGCGCCACTGCCCTTTGTCAAA 2517
QY 2482 ATGTGATGCACATAAGCAGGTATCCAGCATGAAATGTAATTTACTTGGAACTAATTTG 2541
Db 2518 ATGTGATGCACATAAGCAGGTATCCAGCATGAAATGTAATTTACTTGGAACTAATTTG 2577
QY 2542 GAAAGAAATTCCTTCTTAAATCAAAACAAACAAACAAACAAACAAAC 2586
Db 2578 GAAAGAAATTCCTTCTTAAATCAAAACAAACAAACAAACAAACAAAC 2622

RESULT 4
US-09-783-732-3
; Sequence 3, Application US/09783732
; Publication No. US20030054417A1
; GENERAL INFORMATION:
; APPLICANT: Chang, David D.
; APPLICANT: Maui, Raymond S.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: EPITHELIAL PROTEIN LOST IN NEOPLASM
; FILE OF INVENTION: (EPLIN)
; FILE REFERENCE: 10809/003001
; CURRENT APPLICATION NUMBER: US/09/783,732
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 09/658,400
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3650
; TYPE: DNA
; ORGANISM: Homosapien
US-09-783-732-3

Query Match 57.5%; Score 2130; DB 11; Length 3650;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3580; Conservative 0; Mismatches 11; Indels 11; Gaps 4;

QY 92 AGGAAAGCGGCTTTTAGCCAGGTATTTCAGTGTCTGTACAGAGATGGAATCATCTCCA 151
Db 57 AGGAAAGCGGCTTTTAGCCAGGTATTTCAGTGTCTGTACAGAGATGGAATCATCTCCA 116
QY 152 TTTAATAGACGGCAATGGAACCTCTATCATTTAGGCTTAACGCCAAGAACCTTTCTCT 211
Db 117 TTTAATAGACGGCAATGGAACCTCTATCATTTAGGCTTAACGCCAAGAACCTTTCTCT 176
QY 212 GTCAACAGAACAGTCAATCGGCTATTGTGAAATATTCTCCAGTACCAGAAAGCAGCT 271
Db 177 GTCAACAGAACAGTCAATCGGCTATTGTGAAATATTCTCCAGTACCAGAAAGCAGCT 236
QY 272 GAAGAAACAAACATGGAGAAAGAGAGAAATTAACACCGAAATCTCTCCAGCACTTTAGA 331
Db 237 GAAGAAACAAACATGGAGAAAGAGAGAAATTAACACCGAAATCTCTCCAGCACTTTAGA 296
QY 332 AAGGGACCCCTGACTGTGTTTAAAGAAAGTGGGAGAACCCAGGGCTGGGAGCGAGTCT 391
Db 297 AAGGGACCCCTGACTGTGTTTAAAGAAAGTGGGAGAACCCAGGGCTGGGAGCGAGTCT 356
QY 392 CACACAGACTCTTACGGAAACAGCAGCACTGAGATTAGGCACAGCAGACCAATCCTCCT 451
Db 357 CACACAGACTCTTACGGAAACAGCAGCACTGAGATTAGGCACAGCAGACCAATCCTCCT 416
QY 452 GCTGAAGTGACAGGCGCTGCTTCTGGAGCCAAAGCTGACCAAGAGAAACAAATCCAC 511
Db 417 GCTGAAGTGACAGGCGCTGCTTCTGGAGCCAAAGCTGACCAAGAGAAACAAATCCAC 476
QY 512 CCCAGATCTAGACTCAGGTCACTCTCTGAAAGCCCTCGTTTCAAGGTCGATATCCCAATC 571
Db 477 CCCAGATCTAGACTCAGGTCACTCTCTGAAAGCCCTCGTTTCAAGGTCGATATCCCAATC 536

QY 572 AAGGACGCTGAGGATCTTTAAAGACCCTCAACAGAAAGTAAAAAATGAAAAATTTGTCTA 631
Db 537 AAGGACGCTGAGGATCTTTAAAGACCCTCAACAGAAAGTAAAAAATGAAAAATTTGTCTA 596
QY 632 GGAGAAATCCAGGATGAAGTAGAAAAATCAGAAATCAGTGAAGAACACAGATGCTTCGGGC 691
Db 597 GGAGAAATCCAGGATGAAGTAGAAAAATCAGAAATCAGTGAAGAACACAGATGCTTCGGGC 656
QY 692 AAAATAGAGAAATATAATGTTTCGCTGAAACAGGCTTAAGATGATGTTTGAAGAGGTGAA 751
Db 657 AAAATAGAGAAATATAATGTTTCGCTGAAACAGGCTTAAGATGATGTTTGAAGAGGTGAA 716
QY 752 CCAACTCAAACTAGATTTCTCGGGCCCAAGCCGAAGTCAAGTGAAGAACAGATCTCT 811
Db 717 CCAACTCAAACTAGATTTCTCGGGCCCAAGCCGAAGTCAAGTGAAGAACAGATCTCT 776
QY 812 GAAACAGCTATTCTCTAGATGACCTGGAATAGGCCAGGTCAAGTGTCTTCTTACA 871
Db 777 GAAACAGCTATTCTCTAGATGACCTGGAATAGGCCAGGTCAAGTGTCTTCTTACA 836
QY 872 TTTGACTCGGAGAAAAATGAGAGTAGACGAAATCTGGAATCTCCAGGCTCTCAGAAACC 931
Db 837 TTTGACTCGGAGAAAAATGAGAGTAGACGAAATCTGGAATCTCCAGGCTCTCAGAAACC 896
QY 932 TCTATAAAGGATCGAATGGCCCAAGTACAGGCACTGTGTCCAAACAAAGCAGCTCAACC 991
Db 897 TCTATAAAGGATCGAATGGCCCAAGTACAGGCACTGTGTCCAAACAAAGCAGCTCAACC 956
QY 992 AACTATACAAATGAGCTGAAAGCCAGTGGTGGCGAAATCAAAATTCATAAATGAGCAA 1051
Db 957 AACTATACAAATGAGCTGAAAGCCAGTGGTGGCGAAATCAAAATTCATAAATGAGCAA 1016
QY 1052 AAGGAGAAATGTGCCCCCAGGTCCTGAGGTCTGCATCAACCCATCAGGAAGGGGAAAGATT 1111
Db 1017 AAGGAGAAATGTGCCCCCAGGTCCTGAGGTCTGCATCAACCCATCAGGAAGGGGAAAGATT 1076
QY 1112 TCTGCAATGAGATAGCTGCGCAGTCCGTTCCACCCCTGCGGAAGATGACTCCC- -GT 1168
Db 1077 TCTGCAATGAGATAGCTGCGCAGTCCGTTCCACCCCTGCGGAAGATGACTCCCAGGT 1136
QY 1169 GACTCCCAGGTTAAGAGTGAGGTTCAACAGCCTGTCATCCCAAGCCACTAAGTCCAGAT 1228
Db 1137 GACTCCCAGGTTAAGAGTGAGGTTCAACAGCCTGTCATCCCAAGCCACTAAGTCCAGAT 1196
QY 1229 TCCAGAGCTCCAGTCTTTCTGAAAGTTCTCTCTCCAAAGCAATCAAGAAAGTTTCAGGCA 1288
Db 1197 TCCAGAGCTCCAGTCTTTCTGAAAGTTCTCTCTCCAAAGCAATCAAGAAAGTTTCAGGCA 1256
QY 1289 CTTGCAAGAGAGACCTGCGTGGAAATGTGAGAGACAGTCTATCCAAATGGAGGCTCTCTG 1348
Db 1257 CTTGCAAGAGAGACCTGCGTGGAAATGTGAGAGACAGTCTATCCAAATGGAGGCTCTCTG 1316
QY 1349 GCCAACAGCAGGTTTTCAGATCAGCTGCTTCGTTGCTCCTATTGCAACAAACAACTC 1408
Db 1317 GCCAACAGCAGGTTTTCAGATCAGCTGCTTCGTTGCTCCTATTGCAACAAACAACTC 1376
QY 1409 AGTCTAGGAACATATGCACTTTTACATGGAAGAAATCTATTGTAAGCCTCACTTCAATCAA 1468
Db 1377 AGTCTAGGAACATATGCACTTTTACATGGAAGAAATCTATTGTAAGCCTCACTTCAATCAA 1436
QY 1469 CTCCTTTAAATCTAAGGGCAACTATGATGAAGGCTTTGGGCACAGACCAACAAAGATCTA 1528
Db 1437 CTCCTTTAAATCTAAGGGCAACTATGATGAAGGCTTTGGGCACAGACCAACAAAGATCTA 1496
QY 1529 TGGGCAAGCAAAATGAAAAACGAAAGATTTTGGAGAGACCCAGCCAGCTTGCATATGCA 1588
Db 1497 TGGGCAAGCAAAATGAAAAACGAAAGATTTTGGAGAGACCCAGCCAGCTTGCATATGCA 1556
QY 1589 AGGAGACCCCTCAGAGCCAGGGGTAGAGATGCCCTATTGCTAAGGTGGGTGCTCCTG 1648
Db 1557 AGGAGACCCCTCAGAGCCAGGGGTAGAGATGCCCTATTGCTAAGGTGGGTGCTCCTG 1616

1649 GCTGCAAGTATGGAAGCAAGCCCTCTCTCAGCAGGAGAGAGAGCAAGCCAGCTGAA 1708
1617 GCTGCAAGTATGGAAGCAGGAGCCCTCTCTCAGCAGGAGAGAGAGCAAGCCAGCTGAA 1676
1709 ACCAAGAGCTGAGGATGCGCTGGCCACCCCTCCACTGAACTTGAAGTTTCAGGAAGTGC 1768
1677 ACCAAGAGCTGAGGATGCGCTGGCCACCCCTCCACTGAACTTGAAGTTTCAGGAAGTGC 1736
1769 TTGGAGGAAGGATCAAAATGTCAAGGCCAAATGGCCCTCTGAGAGCAAAATCAGCAAG 1828
1737 TTGGAGGAAGGATCAAAATGTCAAGGCCAAATGGCCCTCTGAGAGCAAAATCAGCAAG 1796
1829 CCCGAAGTCTGAGGATGCTGATCTAGATCTGAAGAAGCTAAGACGATCTTCTTCACTG 1888
1797 CCCGAAGTCTGAGGATGCTGATCTAGATCTGAAGAAGCTAAGACGATCTTCTTCACTG 1856
1889 AAGGAAGAGCGGCCCATCTCACTGTAGCAGCTTCAATTTCAAAGCACCTCTGTCAAGAGC 1948
1857 AAGGAAGAGCGGCCCATCTCACTGTAGCAGCTTCAATTTCAAAGCACCTCTGTCAAGAGC 1916
1949 CCAAAACCTGTGTCCCACTATCAGGAAGGCTGGAGCATGTGAGAGCAAGAGCAAG 2008
1917 CCAAAACCTGTGTCCCACTATCAGGAAGGCTGGAGCATGTGAGAGCAAGAGCAAG 1976
2009 TCTGTGGTGGAGAGTTGCGAAGAGCAAGTGGMAAATGCCAAGGCTTCTTAAGAG 2068
1977 TCTGTGGTGGAGAGTTGCGAAGAGCAAGTGGMAAATGCCAAGGCTTCTTAAGAG 2036
2069 AATGGGAATGTGGGAAACCAACCTGGCAAAACAAAGAACTCTAAAGGAGAGCAGGGAAG 2128
2037 AATGGGAATGTGGGAAACCAACCTGGCAAAACAAAGAACTCTAAAGGAGAGCAGGGAAG 2096
2129 AGAAGTAAGGAAGTGTATAGTTGGAGATGGAGAATGAGAATCTTGTGAAATGTTGCA 2188
2097 AGAAGTAAGGAAGTGTATAGTTGGAGATGGAGAATGAGAATCTTGTGAAATGTTGCA 2156
2189 GACTCCGATGAAGATGAATACAGCTTCTCAACACAACTCTCAAGAACCCAGTCT 2248
2157 GACTCCGATGAAGATGAATACAGCTTCTCAACACAACTCTCAAGAACCCAGTCT 2216
2249 CTGAATGTGTGAGTTGTAGACCAACCTTGTGAGCAATCTACTCTAGAATCAG 2308
2217 TTGAATGTGTGAGTTGTAGACCAACCTTGTGAGCAATCTACTCTAGAATCAG 2276
2309 AATCCCGAGATGGAACCTCTGGAGGAGAGTGGTCAAGAGCTCTCTGTGGAAGAA 2368
2277 AATCCCGAGATGGAACCTCTGGAGGAGAGTGGTCAAGAGCTCTCTGTGGAAGAA 2336
2369 CAGATAAAGAGAAATCGGTATATGATGAGATGAGATGAAGATGCAAAATGCAATG 2428
2337 CAGATAAAGAGAAATCGGTATATGATGAGATGAGATGAAGATGCAAAATGCAATG 2396
2429 ATGTGGGCCCTTAAATTCATGTTAGTGTAGCGAGCCACTGCCCTTTGTCAAAATGTGAT 2488
2397 ATGTGGGCCCTTAAATTCATGTTAGTGTAGCGAGCCACTGCCCTTTGTCAAAATGTGAT 2456
2489 GCACATAGCAGGATCCACGATGAATGTAATTTACTTGGAGTAACTTTGGAAGAAGA 2548
2457 GCACATAGCAGGATCCACGATGAATGTAATTTACTTGGAGTAACTTTGGAAGAAGA 2516
2549 ATTCTCTCTTAAATCAAAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAA 2608
2517 ATTCTCTCTTAAATCAAAAAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAA 2576
2609 AGATAACTTTTACTTAAATCTTCAATTTAGCAGTGAATGATGATGATGATGATGATGATGAT 2668
2577 AGATAACTTTTACTTAAATCTTCAATTTAGCAGTGAATGATGATGATGATGATGATGATGAT 2631
2669 TTGTAACCTGGGAAATATTCACCTGATAAATAGCCCAAGTCTACTGTATTTCCCAAGAG 2728
2632 TTGTAACCTGGGAAATATTCACCTGATAAATAGCCCAAGTCTACTGTATTTCCCAAGAG 2691
2729 CAATATTAAAGGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2788

2692 CAATATTAAAGGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2751
2789 AACATACAGAAGAAATTTAGGGGCTTTAAACATTTACGACTGAATGCACTTTTAGTATAAAGG 2848
2752 AACATACAGAAGAAATTTAGGGGCTTTAAACATTTACGACTGAATGCACTTTTAGTATAAAGG 2810
2849 GCACAGTTGTATATTTTAAATGAATACCAATTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2908
2811 GCACAGTTGTATATTTTAAATGAATACCAATTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2870
2909 AGATTATTTAGTCTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 2968
2871 AGATTATTTAGTCTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 2930
2969 TTACTAGCTTTATGTCCTGCTCTCTAAACTACATCTGAACTCGACGCTCTCTGAGGTATAAT 3028
2931 TTACTAGCTTTATGTCCTGCTCTCTAAACTACATCTGAACTCGACGCTCTCTGAGGTATAAT 2988
3029 ACAACAGAGCACCTTTTGGAGCAATTTGAAACCAACCTACCTCTCTCGGTGCTTAGAGA 3088
2989 ACAACAGAGCACCTTTTGGAGCAATTTGAAACCAACCTACCTCTCTCGGTGCTTAGAGA 3048
3089 GATCTGCTGCTCCCAATTAAGCTTTTGTATCTGCCAGTGAATTTACTGACTCCAAATG 3148
3049 GATCTGCTGCTCCCAATTAAGCTTTTGTATCTGCCAGTGAATTTACTGACTCCAAATG 3108
3149 ATTGCTTTCTTTCTGCTGATCTGCTCTCTCATTAATTTACTGAAAGCTCAATATTTT 3208
3109 ATTGCTTTCTTTCTGCTGATCTGCTGCTCTCTCATTAATTTACTGAAAGCTCAATATTTT 3168
3209 AGTAATACCTTTGGGATCACCTGCTCCCTCATCTTCCGTTGTAGACAAAGTGAAGAGTTTA 3268
3169 AGTAATACCTTTGGGATCACCTGCTCCCTCATCTTCCGTTGTAGACAAAGTGAAGAGTTTA 3228
3269 AAGGAGGAAGAAAGAACTGCTTTACACCACTTTGAGCTCAGACCTCTAAACCTGTAT 3328
3229 AAGGAGGAAGAAAGAACTGCTTTACACCACTTTGAGCTCAGACCTCTAAACCTGTAT 3288
3329 TTCCCTTATGATGTCCTTTTGGAGCACTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3388
3289 TTCCCTTATGATGTCCTTTTGGAGCACTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3348
3389 ATATTGATTTTATCACAGTATTTCTCAGGTTGAAATTTAAACCAACTATAGGCTTTTCT 3448
3349 ATATTGATTTTATCACAGTATTTCTCAGGTTGAAATTTAAACCAACTATAGGCTTTTCT 3408
3449 TGGGATGATTTTCTAGTCTTAAAGTTTGGGACATTTAAACTTCAGTACATTTTGTGTA 3508
3409 TGGGATGATTTTCTAGTCTTAAAGTTTGGGACATTTAAACTTCAGTACATTTTGTGTA 3468
3509 CACAGTTGATATTTCCAAATTTGATGATGGGAGGAGGCTCTTTAAGCTGTAGGCTTT 3568
3469 CACAGTTGATATTTCCAAATTTGATGATGGGAGGAGGCTCTTTAAGCTGTAGGCTTT 3528
3569 TCTTTGATGATTTTATGAGATTTAGCTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3628
3529 TCTTTGATGATTTTATGAGATTTAGCTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3588
3629 GCTTTCTTGTCTTACTAGTCTGAAACATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3688
3589 GCTTTCTTGTCTTACTAGTCTGAAACATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3648
3689 TG 3690
3649 TG 3650

RESULT 5
US-09-783-732-1
; Sequence 1, Application US/09783732
; Publication No. US20030054417A1
; GENERAL INFORMATION:

APPLICANT: Chang, David D.
APPLICANT: Maui, Raymond S.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: EPITHELIAL PROTEIN LOST IN NEOPLASM
TITLE OF INVENTION: (EPLIN)
FILE REFERENCE: 10809/003001
CURRENT APPLICATION NUMBER: US/09/783,732
CURRENT FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: 09/658,400
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3543
TYPE: DNA
ORGANISM: Homosapien
us-09-783-732-1

Query Match 55.1%; Score 2041; DB 11; Length 3543;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3371; Conservative 0; Mismatches 11; Indels 10; Gaps 3;
302 AACACCGGAAATCTCTCCAGACACTTTAGAAAGGGGACCCCTGACTGTGTTAAAGAGAAG 361
159 AACACCGGAAATCTCTCCAGACACTTTAGAAAGGGGACCCCTGACTGTGTTAAAGAGAAG 218
362 TGGGAGAACCCAGGCTGGGAGCAGAGTCTCACACAGACTCTCTACGGAAACAGCAGCACT 421
219 TGGGAGAACCCAGGCTGGGAGCAGAGTCTCACACAGACTCTCTACGGAAACAGCAGCACT 278
422 GAGATTAGGCACAGACAGACCACTCTCTGCTGAAAGTGAACGCCACCGTCTTCTGGA 481
279 GAGATTAGGCACAGACAGACCACTCTCTGCTGAAAGTGAACGCCACCGTCTTCTGGA 338
482 GCCAAGGTGACCAAGAGAACAAATCACACCCAGACTTACACTCAGCTCAGCTCCTGAA 541
339 GCCAAGGTGACCAAGAGAACAAATCACACCCAGACTTACACTCAGCTCAGCTCCTGAA 398
542 GCCCTCGTTCAGGTCGATATCCACACATCAAGACGCTGAGGATCTTAAAGACCACTCA 601
399 GCCCTCGTTCAGGTCGATATCCACACATCAAGACGCTGAGGATCTTAAAGACCACTCA 458
602 ACAGAAAGTAAAAAATGAAAAATTTCTAGAGAAATCCAGGCATGAAGTGAAGAAATCA 661
459 ACAGAAAGTAAAAAATGAAAAATTTCTAGAGAAATCCAGGCATGAAGTGAAGAAATCA 518
662 GAAATCAGTGAAACACAGACTCTCGGGCAAAATAGAGAAATATAATGTTCCGCTGAAC 721
519 GAAATCAGTGAAACACAGACTCTCGGGCAAAATAGAGAAATATAATGTTCCGCTGAAC 578
722 AGCCTTAAGATGATGTTTGAAGAGGTGAACCACTCRAAATGAAGATCTCCGGGCCCAA 781
579 AGCCTTAAGATGATGTTTGAAGAGGTGAACCACTCRAAATGAAGATCTCCGGGCCCAA 638
782 AGCAGAGTGAAGTGAAGAGGATCTCTGAAAACAGCTATTTCTAGATCAGCTGGAA 841
639 AGCAGAGTGAAGTGAAGAGGATCTCTGAAAACAGCTATTTCTAGATCAGCTGGAA 698
842 ATAGGCCCCAGGTGAGTGTGATCTTCTGATTTGACTCGGAGAAAAATGAGAGTAGACA 901
699 ATAGGCCCCAGGTGAGTGTGATCTTCTGATTTGACTCGGAGAAAAATGAGAGTAGACA 758
902 AATCTGGAATCTCCAGCCTCTCAGAAACCTCTATAAGAGTGAATGCGCAAGTACCAG 961
759 AATCTGGAATCTCCAGCCTCTCAGAAACCTCTATAAGAGTGAATGCGCAAGTACCAG 818
962 GCAGCTGTGCCAAAACAAAGACGCTCAACCACTATACAAATGAGTGAAGCCAGTGGT 1021
819 GCAGCTGTGCCAAAACAAAGACGCTCAACCACTATACAAATGAGTGAAGCCAGTGGT 878
1022 GGCAGAAATCAAAATTCATAAAATGGAGCAAAAGAGAAATGTGCCCCAGGTCTGAGGTC 1081
879 GGCAGAAATCAAAATTCATAAAATGGAGCAAAAGAGAAATGTGCCCCAGGTCTGAGGTC 938

1082 TGCATCCCATCAGGAAGGGGAAAAATTTCTCAAATGAGAAATAGCCTGGCAGTCCGT 1141
939 TGCATCACCCTATCAGGAAGGGGAAAAATTTCTCAAATGAGAAATAGCCTGGCAGTCCGT 998
1142 TCCACCCCTGCGGAAGATGACTCCC---GTCACTCCCAGGTTAAGAGTGAGGTTCAACAG 1198
999 TCCACCCCTGCGGAAGATGACTCCCAGGTTAAGAGTGAGGTTCAACAG 1058
1199 CCGTCCATCCCAAGCCCACTAAGTCCAGATTTCCAGAGCCTCCAGTCTTCTGAAAGTTCT 1258
1059 CCGTCCATCCCAAGCCCACTAAGTCCAGATTTCCAGAGCCTCCAGTCTTCTGAAAGTTCT 1118
1259 CCGTCCATCCCAAGCCCACTAAGTCCAGATTTCCAGAGCCTCCAGTCTTCTGAAAGTTCT 1318
1119 CCGTCCATCCCAAGCCCACTAAGTCCAGATTTCCAGAGCCTCCAGTCTTCTGAAAGTTCT 1178
1319 AAGACAGTCTATCCCAATGGAGCGTCTCTTGGCCAAACACAGAGAGCTGCGTGGAAATGTCT 1378
1179 AAGACAGTCTATCCCAATGGAGCGTCTCTTGGCCAAACACAGAGAGCTGCGTGGAAATGTCT 1238
1379 TCCGTTGCTCTTATGGCAACCAAACTCAGTCTAGGAACATATGCAATCTTTACATGGA 1438
1239 TCCGTTGCTCTTATGGCAACCAAACTCAGTCTAGGAACATATGCAATCTTTACATGGA 1298
1439 AGAATCTATTTAAGCCTCACTTCAATCAACTCTTTAAATCTAAGGGCAACTATGATGAA 1498
1299 AGAATCTATTTAAGCCTCACTTCAATCAACTCTTTAAATCTAAGGGCAACTATGATGAA 1358
1499 GGCTTTGGGCACAGACCAACAGGATCTATGGCAAGCAAAATGAAACCAAGAGATT 1558
1359 GGCTTTGGGCACAGACCAACAGGATCTATGGCAAGCAAAATGAAACCAAGAGATT 1418
1559 TTGGAGAGACCCAGCCAGCTTGCAATGCAAGGGAGACCCCTCACAGCCAGGGGTAGAA 1618
1419 TTGGAGAGACCCAGCCAGCTTGCAATGCAAGGGAGACCCCTCACAGCCAGGGGTAGAA 1478
1619 GATGCCCTATTCTAAGTGGGTGCTTGGCTGCAAGTATGGAAGCCAGGCTCTCTCT 1678
1479 AATGCCCTATTCTAAGTGGGTGCTTGGCTGCAAGTATGGAAGCCAGGCTCTCTCT 1538
1679 CAGCAGGAGAGAGACCAAGCCAGCTGAAACCAAGAGCTGAGGATCGCTCGCCACCC 1738
1539 CAGCAGGAGAGAGACCAAGCCAGCTGAAACCAAGAGCTGAGGATCGCTCGCCACCC 1598
1739 CCACCTGAACTTGGAAAGTTCAGGAAGTCCCTTGGAGGAAGGATCAAAATGTCAAAGCCC 1798
1599 CCACCTGAACTTGGAAAGTTCAGGAAGTCCCTTGGAGGAAGGATCAAAATGTCAAAGCCC 1658
1799 AAATGGCTCTCTGAAGACGAAATCAGCAAGCCGAAAGTTCCTGAGGATGTCGATCTAGAT 1858
1659 AAATGGCTCTCTGAAGACGAAATCAGCAAGCCGAAAGTTCCTGAGGATGTCGATCTAGAT 1718
1859 CTGAAGAGCTTGAAGACGAAATCAGCAAGCCGAAAGTTCCTGAGGATGTCGATCTAGAT 1918
1719 CTGAAGAGCTTGAAGACGAAATCAGCAAGCCGAAAGTTCCTGAGGATGTCGATCTAGAT 1778
1919 GCTTCATTTCAGAGCACTCTGTCAAGAGCCCAAAATCTGTGTCCCAACCTATCAGGAAA 1978
1779 GCTTCATTTCAGAGCACTCTGTCAAGAGCCCAAAATCTGTGTCCCAACCTATCAGGAAA 1838
1979 GGCTGGAGCATGTGAGAGCAGAGTGAAGAGTCTGTGGTGGAAAGAGTTCGAGAAAGAAA 2038
1839 GGCTGGAGCATGTGAGAGCAGAGTGAAGAGTCTGTGGTGGAAAGAGTTCGAGAAAGAAA 1898
2039 CAAGTGGAAAAATGCCAAGGCTTCTAAGAGAAATGGGAAATGGGAAAAAACAACCTGGCAA 2098
1899 CAAGTGGAAAAATGCCAAGGCTTCTAAGAGAAATGGGAAATGGGAAAAAACAACCTGGCAA 1958
2099 AACAAGAAATCTAAGAGGAGACACAGGAGAGTGAAGAGTGAAGAGTCTAGTTTGGAGATG 2158
1959 AACAAGAAATCTAAGAGGAGACACAGGAGAGTGAAGAGTGAAGAGTCTAGTTTGGAGATG 2018

		Matches	473;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
1276	GAAGTTTCAGGACCTGCAAGAGAGACCTGCGTGGAAATGTCAGAGACAGTCTATCCAAAT	1335									
181	GAAGTTTCAGGACCTGCAAGAGAGACCTGCGTGGAAATGTCAGAGACAGTCTATCCAAAT	240									
1336	GGAGCGTCTTGGCCAAACAGCAGAGTGTTCACATCAGCTGCTCCGTTGTCCTATTG	1395									
241	GGAGCGTCTTGGCCAAACAGCAGAGTGTTCACATCAGCTGCTCCGTTGTCCTATTG	300									
1396	CAACAACAACTCAGTCTAGGAACATATGATCTTTACATGGAAGATCTATTGTAAGCC	1455									
301	CAACAACAACTCAGTCTAGGAACATATGATCTTTACATGGAAGATCTATTGTAAGCC	360									
1456	TCACCTCAATCAACTCTTTAAATCTAAGGCAACTATGATGAAGCTTTGGGCACAGACC	1515									
361	TCACCTCAATCAACTCTTTAAATCTAAGGCAACTATGATGAAGCTTTGGGCACAGACC	420									
1516	ACACAAGGATCTATGGCAAGCAAAATGAAAGCAAGAGATTTTGGAGAGACAGCCCA	1575									
421	ACACAAGGATCTATGGCAAGCAAAATGAAAGCAAGAGATTTTGGAGAGACAGCCCA	480									
1576	GTTTCAATCAAGGAGACCCCTCACAGCCAGGGGTAGAAGATGCCCTATTGCTAA	1635									
481	GTTTCAATCAAGGAGACCCCTCACAGCCAGGGGTAGAAGATGCCCTATTGCTAA	540									
1636	GTTGGGTGCTCCTGGCTGCAAGTATGAAGCCAGGCTCTCTCAGCAGGAGAGGAAGA	1695									
541	GTTGGGTGCTCCTGGCTGCAAGTATGAAGCCAGGCTCTCTCAGCAGGAGAGGAAGA	600									
1696	CAAGCCAGCTGAAACCAAGAGCTGAGGATCGCTGCGCCACCCACCTGAACTTGGAG	1755									
601	CAAGCCAGCTGAAACCAAGAGCTGAGGATCGCTGCGCCACCCACCTGAACTTGGAG	660									
1756	TTCAAGAGTGCCTTCGAGGAAGGATCAAAATGTCAGAGCCCAATGG	1804									
661	TTCAAGAGTGCCTTCGAGGAAGGATCAAAATGTCAGAGCCCAATGG	709									

RESULT 7
US-10-066-543-3200
; Sequence 3200, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margrita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3200
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 533
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-3200

Query Match 11.4%; Score 423; DB 15; Length 547;
Best Local Similarity 99.8%; Pred. No. 4.5e-192;
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1276	GAAGTTTCAGGACCTGCAAGAGAGACCTGCGTGGAAATGTCAGAGACAGTCTATCCAAAT	1335
DB	181	GAAGTTTCAGGACCTGCAAGAGAGACCTGCGTGGAAATGTCAGAGACAGTCTATCCAAAT	240
QY	1336	GGAGCGTCTTGGCCAAACAGCAGAGTGTTCACATCAGCTGCTCCGTTGTCCTATTG	1395
DB	241	GGAGCGTCTTGGCCAAACAGCAGAGTGTTCACATCAGCTGCTCCGTTGTCCTATTG	300
QY	1396	CAACAACAACTCAGTCTAGGAACATATGATCTTTACATGGAAGATCTATTGTAAGCC	1455
DB	301	CAACAACAACTCAGTCTAGGAACATATGATCTTTACATGGAAGATCTATTGTAAGCC	360
QY	1456	TCACCTCAATCAACTCTTTAAATCTAAGGCAACTATGATGAAGCTTTGGGCACAGACC	1515
DB	361	TCACCTCAATCAACTCTTTAAATCTAAGGCAACTATGATGAAGCTTTGGGCACAGACC	420
QY	1516	ACACAAGGATCTATGGCAAGCAAAATGAAAGCAAGAGATTTTGGAGAGACAGCCCA	1575
DB	421	ACACAAGGATCTATGGCAAGCAAAATGAAAGCAAGAGATTTTGGAGAGACAGCCCA	480
QY	1576	GTTTCAATCAAGGAGACCCCTCACAGCCAGGGGTAGAAGATGCCCTATTGCTAA	1635
DB	481	GTTTCAATCAAGGAGACCCCTCACAGCCAGGGGTAGAAGATGCCCTATTGCTAA	540
QY	1636	GTTGGGTGCTCCTGGCTGCAAGTATGAAGCCAGGCTCTCTCAGCAGGAGAGGAAGA	1695
DB	541	GTTGGGTGCTCCTGGCTGCAAGTATGAAGCCAGGCTCTCTCAGCAGGAGAGGAAGA	600
QY	1696	CAAGCCAGCTGAAACCAAGAGCTGAGGATCGCTGCGCCACCCACCTGAACTTGGAG	1755
DB	601	CAAGCCAGCTGAAACCAAGAGCTGAGGATCGCTGCGCCACCCACCTGAACTTGGAG	660
QY	1756	TTCAAGAGTGCCTTCGAGGAAGGATCAAAATGTCAGAGCCCAATGG	1804
DB	661	TTCAAGAGTGCCTTCGAGGAAGGATCAAAATGTCAGAGCCCAATGG	709

RESULT 8
US-10-060-036-4338
; Sequence 4338, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4338
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 416, 418, 556
; OTHER INFORMATION: n = A,T,C or G
US-10-060-036-4338

Query Match 11.2%; Score 415; DB 15; Length 565;
Best Local Similarity 100.0%; Pred. No. 1.1e-188;
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1295	TTTCAAGCACCTCTGTCAAGAGCCCAAAACTGTGTCCCGCTATCAGGAAAGGCTGG	1984
DB	1	TTTCAAGCACCTCTGTCAAGAGCCCAAAACTGTGTCCCGCTATCAGGAAAGGCTGG	60
QY	1985	ACCATCTCAGACGACAGTGAAGAGTCTGTGGTGAAGAGTTCAGAAAGAAACAGTG	2044

Query Match	10.4%	Score 385;	DB 15;	Length 698;
Best Local Similarity	100.0%;	Pred. No. 2.9e-174;		
Matches 385;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
302	AACACCCGAAAAATCTCTCCGAGCACTTTAGAAAGGGGACCCCTGACTGTGTTAAAGAGAAG	361		
Db	293	AACACCCGAAAAATCTCTCCGAGCACTTTAGAAAGGGGACCCCTGACTGTGTTAAAGAGAAG	352	
Qy	362	TGGAGAGAACCCAGGGCTGGGAGCAGAGTCTTCACAGACTCTCTACGGAAACAGCAGCACT	421	
Db	353	TGGAGAGAACCCAGGGCTGGGAGCAGAGTCTTCACAGACTCTCTACGGAAACAGCAGCACT	412	
Qy	422	GAGATTAGGCACAGAGCAGACCACTCTCTGCTGAAAGTGAACAGCCACGCTCTCTCGA	481	
Db	413	GAGATTAGGCACAGAGCAGACCACTCTCTGCTGAAAGTGAACAGCCACGCTCTCTCGA	472	
Qy	482	GCCAAAGCTGACCAAGAGAACAAATCCACCCAGACTCTAGACTCAGGTCACTCTCTGAA	541	
Db	473	GCCAAAGCTGACCAAGAGAACAAATCCACCCAGACTCTAGACTCAGGTCACTCTCTGAA	532	
Qy	542	GCCTCGTTCAGGGTCGATATCCCAATCAAGSACGGTGAGGATCTTAAAGACCACTCA	601	
Db	533	GCCTCGTTCAGGGTCGATATCCCAATCAAGSACGGTGAGGATCTTAAAGACCACTCA	592	

```

; SEQ ID NO 3373
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 534
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-3373

Query Match          10.8%; Score 401; DB 15; Length 583;
Best Local Similarity 99.8%; Pred. NO. 5.8e-182;
Matches 451; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2586 AAAAAACACATTCCTAAATCTAGAGATAACTTTTACTTTAAATCTTCATTTTACAGCTGAT 2645
      |||||
Db 35 AAAAAACACATTCCTAAATCTAGAGATACTTTTACTTTAAATCTTCATTTTACAGCTGAT 94

QY 2646 GATATGCATAAGTGTCTGAAGCGTTGTAACTGGGGAAATATTCACCTGATATAGCCCA 2705
      |||||
Db 95 GATATGCATAAGTGTCTGAAGCGTTGTAACTGGGGAAATATTCACCTGATATAGCCCA 154

QY 2706 GATTCCTACTGTATTCCTCCAAAGGCGAATATTAAAGGTAGATAGATGATTAGTAGTATATTGT 2765
      |||||
Db 155 GATTCCTACTGTATTCCTCCAAAGGCGAATATTAAAGGTAGCAGATGATTAGTAGTATATTGT 214

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602 ACAGAAAGTAAAAAATGAAAATTTCTAGGAGATCCAGGATGAAAGTAGAAAAATCA 661
603 ACAGAAAGTAAAAAATGAAAATTTCTAGGAGATCCAGGATGAAAGTAGAAAAATCA 662
604 ACAGAAAGTAAAAAATGAAAATTTCTAGGAGATCCAGGATGAAAGTAGAAAAATCA 663
605 ACAGAAAGTAAAAAATGAAAATTTCTAGGAGATCCAGGATGAAAGTAGAAAAATCA 664
606 GAAATCAGTGAAGAACACAGATGCTT 686
607 GAAATCAGTGAAGAACACAGATGCTT 677
608 GAAATCAGTGAAGAACACAGATGCTT 678
609 GAAATCAGTGAAGAACACAGATGCTT 679
610 GAAATCAGTGAAGAACACAGATGCTT 680

RESULT 11
JS-09-871-161-139/c
; Sequence 139, Application US/09871161
; Publication No. US20030097666A1
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCNA-260X
; CURRENT APPLICATION NUMBER: US/09/871,161
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 09/328,111
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/117,393
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/098,639
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 139
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(586)
; OTHER INFORMATION: n = A,T,C or G

US-09-871-161-139
Query Match 9.8%; Score 362; DB 11; Length 586;
Best Local Similarity 100.0%; Pred. No. 3.3e-163;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3137 GTACTCCAAATGATTGCTTTCTTTCTGGTGATATCTGTGCTCTCATATTAATCTGAAG 3196
DB 363 GTACTCCAAATGATTGCTTTCTTTCTGGTGATATCTGTGCTCTCATATTAATCTGAAG 304
QY 3197 CTGCAATATTTAGTAAATACCTTCGGGATCACTGCCCCCATCTTCGGTGTTAGAGCAAA 3256
DB 303 CTGCAATATTTAGTAAATACCTTCGGGATCACTGCCCCCATCTTCGGTGTTAGAGCAAA 244
QY 3257 GTGAAGAGTTTAAAGGAGGAGAAAGAAAGAACTGCTTACACCACTTCGAGCTCAGACCTC 3316
DB 243 GTGAAGAGTTTAAAGGAGGAGAAAGAAAGAACTGCTTACACCACTTCGAGCTCAGACCTC 184
QY 3317 TAAACCTGATTTCCCTTTATGATGTCCTTTTGGAGACATAATTTTAAATACCTTAC 3376
DB 183 TAAACCTGATTTCCCTTTATGATGTCCTTTTGGAGACATAATTTTAAATACCTTAC 124
QY 3377 TAGCTCTGAAATATATGATTTTATCAGATATTCAGGGTGAAATTAACCAACTAT 3436
DB 123 TAGCTCTGAAATATATGATTTTATCAGATATTCAGGGTGAAATTAACCAACTAT 64
QY 3437 AGGCTTTTCTTGGGATGATTTTCTAGTCTTAAAGTTTGGGACATTTAAACTTGAGT 3496
DB 63 AGGCTTTTCTTGGGATGATTTTCTAGTCTTAAAGTTTGGGACATTTAAACTTGAGT 4
QY 3497 AC 3498
DB 3 AC 2

RESULT 12
US-10-066-543-1533/c

Sequence 1533, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Pye, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1533
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-066-543-1533
Query Match 9.7%; Score 358; DB 15; Length 358;
Best Local Similarity 100.0%; Pred. No. 2.7e-161;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3139 ACTCCAAATGATTGCTTTCTTTCTGGTGATATCTGTGCTCTCATATTAATCTGAAGCT 3198
DB 358 ACTCCAAATGATTGCTTTCTTTCTGGTGATATCTGTGCTCTCATATTAATCTGAAGCT 299
QY 3199 GCAATATTTTAGTAATACCTTCGGGATCACTGCCCCCATCTTCGGTGTTAGAGCAAACT 3258
DB 298 GCAATATTTTAGTAATACCTTCGGGATCACTGCCCCCATCTTCGGTGTTAGAGCAAACT 239
QY 3259 GAAGAGTTTAAAGGAGGAGAAAGAAAGAACTGCTTACACCACTTCGAGCTCAGACCTCTA 3318
DB 238 GAAGAGTTTAAAGGAGGAGAAAGAAAGAACTGCTTACACCACTTCGAGCTCAGACCTCTA 179
QY 3319 AACCTGTATTTCCCTTTATGATGTCCTTTTGGAGACATAATTTTAAATACTTACTA 3378
DB 178 AACCTGTATTTCCCTTTATGATGTCCTTTTGGAGACATAATTTTAAATACTTACTA 119
QY 3379 GCTCTCAATATATTCATTTTATCAGATATTCAGGGTAAATTAACCAACTATAG 3438
DB 118 GCTCTCAATATATTCATTTTATCAGATATTCAGGGTAAATTAACCAACTATAG 59
QY 3439 GCCTTTTCTTGGGATGATTTTCTAGTCTTGGGACATTTAAACTTGAGT 3496
DB 58 GCCTTTTCTTGGGATGATTTTCTAGTCTTGGGACATTTAAACTTGAGT 1
RESULT 13
US-09-796-692-2900
; Sequence 2900, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algete, Paul A.
; APPLICANT: Marion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17

PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2900
LENGTH: 262
TYPE: DNA
ORGANISM: Homo sapiens
US-10-040-862-2900

Query Match 6.8%; Score 253; DB 15; Length 262;
Best Local Similarity 100.0%; Pred. No. 8.7e-111;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3440 CCTTTTCTGGGATGATTTCTAGCTTTAGGTTGGGACATTTAACTTGGATGTA 3499
DB 1 CCTTTTCTGGGATGATTTCTAGCTTTAGGTTGGGACATTTAACTTGGATGTA 60
Y 3500 TTGTTGTACACAGTTGATATTCCTAAATTTGATGGGAGGAGGTGCTTTAAAGCT 3559
DB 61 TTGTTGTACACAGTTGATATTCCTAAATTTGATGGGAGGAGGTGCTTTAAAGCT 120
Y 3560 GTAGGCTTTCTTTGTACTGCATTTATAGAGATTTAGCTTTTAAATTTTATAGAGATGTA 3619
DB 121 GTAGGCTTTCTTTGTACTGCATTTATAGAGATTTAGCTTTTAAATTTTATAGAGATGTA 180
Y 3620 AAACATTCGCTTTCTAGCTTTACCTAGTCTGAACATTTTATTCATTAAGATTTTA 3679
DB 181 AAACATTCGCTTTCTAGCTTTACCTAGTCTGAACATTTTATTCATTAAGATTTTA 240
Y 3680 ATTAATAATTTGAA 3692
DB 241 ATTAATAATTTGAA 253

RESULT 15
US-10-198-846-8531/c
Sequence 8531, Application US/10198846
Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0

PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 9597
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2900
LENGTH: 262
TYPE: DNA
ORGANISM: Homo sapiens
US-09-796-692-2900

Query Match 6.8%; Score 253; DB 10; Length 262;
Best Local Similarity 100.0%; Pred. No. 8.7e-111;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3440 CCTTTTCTGGGATGATTTCTAGCTTTAGGTTGGGACATTTAACTTGGATGTA 3499
DB 1 CCTTTTCTGGGATGATTTCTAGCTTTAGGTTGGGACATTTAACTTGGATGTA 60
Y 3500 TTGTTGTACACAGTTGATATTCCTAAATTTGATGGGAGGAGGTGCTTTAAAGCT 3559
DB 61 TTGTTGTACACAGTTGATATTCCTAAATTTGATGGGAGGAGGTGCTTTAAAGCT 120
Y 3560 GTAGGCTTTCTTTGTACTGCATTTATAGAGATTTAGCTTTTAAATTTTATAGAGATGTA 3619
DB 121 GTAGGCTTTCTTTGTACTGCATTTATAGAGATTTAGCTTTTAAATTTTATAGAGATGTA 180
Y 3620 AAACATTCGCTTTCTAGCTTTACCTAGTCTGAACATTTTATTCATTAAGATTTTA 3679
DB 181 AAACATTCGCTTTCTAGCTTTACCTAGTCTGAACATTTTATTCATTAAGATTTTA 240
Y 3680 ATTAATAATTTGAA 3692
DB 241 ATTAATAATTTGAA 253

RESULT 14
US-10-040-862-2900
Sequence 2900, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545